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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Mar 7 21:10:00 2000; MasPar time 3.88 Seconds 122.160 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-981-824-1

(1-20) from US08981824 pep 146 1 DVNYAFLHATDLLPACDGER 20 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

188963 segs, 23686106 Minimum Match 08, Listing first 45 Post-processing:

Searched:

residues

summaries

Database:

-geneseq35 1:geneseqp Mean-20.820; Statistics:

Variance 63.757; scale 0.327

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADTES

		ď			SUMMARIES		
Result		Query					
. P	Score	Match	Length	BB :	ID	Description	Pred. No.
н	146	100.0	20	۲	W01793	Human 65 kD glutamine	4.60e-09
7	146	100.0	20	Н	W18842	65 kD Glutamic acid de	4.60e-09
m	146	100.0	503	-	R23645	Human GAD65 gene produ	4.60e-09
4	146	100.0	540	-1	R59520		4.60e-09
Ŋ	146	100.0	544	-	R59524	GAD65 545-585 C-termin	4.60e-09
φ	146	100.0	554	٦	R59518	GAD65 1-31 deleted, C4	4.60e-09
7	146	100.0	584	٦	W86017	Human GAD65 protein se	4.60e-09
œ	146	100.0	584	-	W34519	Human GAD65 protein.	4.60e-09
თ	146	100.0	585	Н	W12402		4.60e-09
10	146	100.0	585	-1	W14915	Modified glutamic acid	4.60e-09
11	146	100.0	585	Н	R28756	Human pancreatic islet	4.60e-09
12	146	100.0	585	Н	R59516	Human GAD65.	4.60e-09
13	146	100.0	585	٦	R79105	Human glutamic acid de	4.60e-09
14	146	100.0		1	W14916	Modified glutamic acid	4.60e-09
15	146	100.0		~	R71641	Human GAD.	4.60e-09
16	146	100.0	585	-	R29629	Human GAD 65.	4.60e-09
17	146	100.0	585		W35361	Human 65K-glutamic aci	4.60e-09
18	135	92.5	585		R23644	Rat GAD65 gene product	1.07e-07
19	135	92.5	585	Н	R29628	Rat GAD 65.	1.07e-07
20	135	92.5	605	-	R71733	Rat glutamic acid deca	1.07e-07
21	129	88.4	584	Н	W85018	Rat GAD65 protein segu	, 5.88e-07
22	129	88.4	584	Н	W34520		5.88e-07
23	128	87.7	540	٦	R59521	GAD65 1-45 N-terminal-	7.80e-07

24 128 87.7 544 1 R59525 GAD65 1-31 deleted, C4 7.80e-07 25 128 87.7 584 1 R59519 GAD65 1-31 deleted, C4 7.80e-07 27 29 67.8 14 1 W18654 Peptide derived from h 7.80e-07 29 67.8 14 1 W18654 Peptide derived from h 2.38e-03 29 67.8 14 1 W18657 Glutamic acid decarbox 1.19e-02 30 63.7 20 1 R72266 Glutamic acid decarbox 1.19e-02 31 61 41.8 593 1 R7226 Glutamic acid decarbox 1.19e-02 32 61 41.8 594 1 R7222 Glutamic acid decarbox 1.19e-02 34 41.8 594 1 R7722 Brain GAD #2. 4.01e+01 35 61 41.8 594 1 W7471 Amino acid sequence of 4.01e+01 36 61 41.8 594 1 W7471 Amino acid sequence of 4.01e+01 36 <td< th=""></td<>
128 87.7 544 1 R59525 GAD65 1-31 deleted 128 87.7 585 1 R59519 GAD65 1-31 deleted 128 87.7 585 1 R59519 R4 GAD65 1-31 deleted 128 87.7 585 1 R59517 Reptide derived from 14 1 W18857 Febtide derived from 14 1 W18857 Glutamic acid deca 63 43.2 53 1 R7226 Glutamic acid deca 63 43.2 53 1 R7226 E.coli malate synt 61 41.8 594 1 R7220 Brain GAD #2. and 14.8 594 1 W74716 Amino acid sequence 61 41.8 594 1 W74717 Full length brain 61 41.8 594 1 W74717 Full length brain 61 41.8 594 1 W74717 Full length islet 61 41.8 66 1 W31266 Mutine Apinol (a-3.7) 198 19.7 39.7 190 1 R98922 Mutine Apinol (a-3.7) 188 189.7 190 1 R98922 Human G-protein co 58 39.7 424 1 R6341 Mutine Apinol Aridae 58 39.7 653 1 R40923 Alcohol Anian acid sequence 58 39.7 653 1 R40923 Alcohol Anianse Froeptor WE2 57 39.0 848 1 R80551 Human Ah receptor WE2 57 39.0 2707 1 W27161 Mouse receptor WE2
128 87.7 554 1 128 87.7 554 1 99 67.8 14 1 99 67.8 14 1 99 67.8 14 1 61 41.8 593 1 61 41.8 594 1 61 58 39.7 573 1 58 39.7 653 1 58 39.7 653 1 57 39.0 270 1
128 87.7 554 128 87.7 554 128 87.7 554 99 67.8 14 99 67.8 14 67.8 120 63.7 20 63.7 20 63.4 43.2 20 61 41.8 594 61 41.8 594 61 41.8 594 61 41.8 594 61 41.8 594 61 41.8 594 61 42.8 39.7 273 58 39.7 424 58 39.7 423 58 39.7 424 58 39.7 665 57 39.0 2707
128 87.7 128 87.7 128 87.7 99 967.8 87.7 93 653.7 61 41.8 61 61 61 61 61 61 61 61 61 61 61 61 61 6
1128 1288 1288 1288 1399 100 110 101 101 101 101 101 101 101 1
77777777777777777777777777777777777777

ALIGNMENTS

MUT 1993; Carrier on try)

DE 7:19-0CT-1997 (first entry)

E Human 65 kD glutamine decarboxylase peptide.

E Human 65 kD glutamine decarboxylase peptide.

E Human 65 kD glutamine decarboxylase; GAD: diagnosis; predisposition; kW tumour; immunological; disease; autoimmune; diabetes; reagent; kW determination; T cell; subpopulation; medicament; treatment; kW reinjection; inactivation.

S HOMO sapiens.

D HOMO sapiens.

P H -JUL-1995; DE-025784.

P H -JUL-1995; DE-025784.

P H -JUL-1995; DE-025784.

P R L -JUL-1995; DE-025784.

P R H diabetes, etc. 15pp; German.
Claim 1; Page 12; 15pp; German.
The present peptide is a framgent of the human 65 kD glutamine decarboxylase (GAD), which can be used to diagnose, or diagnose a predisposition to, a tumnour or immunological disease, preferably an autoimmune disease, especially diabetes. It can also be used as a reagent to determine specific T cell subpopulations, in medicaments to treat or prevent immunological diseases, preferably autoimmune diseases, especially diabetes, to produce antigens, especially immunogens or tolerogens and to isolate specific T cell subpopulations, which can be used to produce antigens or for reinjection, optionally after inactivation. W01793 standard; peptide; 20 AA. W01793; RESULT ID WO AC WO

ö Match 100.0%; Score 146; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 4.60e-09; es 20; Conservative 0; Mismatches 0; Indels Query Match Best Local S: Matches 20

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Gaps

1 DVNYAFLHATDLLPACDGER 20

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RESULT 2 ID W18842 standard; peptide; 20 AA. AC W18842; DT 05-JAN-1998 (first entry)



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                                                                                                                                                                                                                                          Involving intradermal admin. Of mutoireactive substances involving intradermal admin. Of mutoireactive substances Claim 11; Page 9; 12pp; German.

W18842-70 are peptide fragments of the 65 kD human glutamic acid decarboxylase (GAD). The fragments are autoreactive substances used for diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is determined by using a claimed method for diagnosis of cell-mediated diseases. Which is effected by administering an autoreactive substance intradermally and establishing the diagnosis on the basis of the occurrence or lack of a positive reaction at the site of administration. The method is used for diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated diseases such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
65 kD Glutamic acid decarboxylase peptide fragment I. Ash. 65 kD; human; glutamic acid decarboxylase, autoreactive; diagnosis; insulin-dependent diabetes mellitus; IDDM; cell-mediated disease; predisposition; autoimmune; tumour; rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence given is a glutamic acid decarboxylase (GAD65). GAD65 can be used for the diagnosis and therapy of patients with autoimmune diseases, esp. insulin-dependant diabetes mellitus (IDDM) and "stiff man" syndrome. It is possible to use either the entire GAD65 protein or polypeptide fragments of it for the immunological detection of autoantibodies to GAD65 which are indicative of IDDM and other auto-immune diseases. The production of this sequence by recombinant DNA technology allows large scale production of eukaryotic GAD65 in its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      native from without the need for separation form other proteinaceous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for therapeutic and diagnostic application in insulin-dependent diabetes mellitus patients
                                                                                                                                                            (BOEF) BOEHRINGER MANNHEIM GMBH.

Donie F. Endl J. Ganz M. Jung G. Kientsch-engel R.;

Pozzilli P. Stahl P.

WPI: 97-088284/09.

Skin test for diagnosis of cell-mediated diseases, esp. diabetes
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Pred. No. 4.60e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GAD65 gene product.
Glutamic acid decarboxylase; IDDM; stiff man syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1992.
23-SEP-1991; 006872.
21-SEP-1990; US-586536.
(REGC ) UNIV CALIFORNIA.
(REGC ) UNIV OR CALIFORNIA.
(REGC ) UNIV OF CALIFORNIA.
ELIANGER MG, RAUFMAN DL, TODIN AJ;
WPI; 92-150489/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R23645 standard; Protein; 503 AA.
R23645;
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Local Similarity 100.0%;
hes 20; Conservative
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                                                                                                              20-JUL-1995, 026561.
20-JUL-1995, DE-026561.
                                                                              Synthetic.
DE19526561-AI
                                                                multiple sclerosis
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Disclosure: Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. The C-terminally deleted mutants given in R59524-25 are able to recognize IDDM autoantibodies having the specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for different classes of GAD65 autoantibodies.
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Disclosure; Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD6 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 146; DB 1; Length 540; Best Local Similarity 100.0%; Pred. No. 4.60e-09; Matches 20; Conservative, 0; Mismatches 0; Indels
                           Indels
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                                                                                                                                                                                                                                                                   GAD65 1-45 N-terminal-deléted mutant.
GAD65; glutamate-decarboxylase; diabetes mellitus;
stiff man syndrome; autoantibody; mutagenesis.
Best Local Similarity 100.0%; Pred. No. 4.60e-09; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1994 (first entry)
GAD65 545-585 C-terminal-deleted mutant.
GAD65; glutamate-decarboxylase; diabetes melli
stiff man syndrome; autoantibody; mutagenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 544 AA
                                                                                                                                                                                                  R59520 standard; protein; 540
R59520;
                                                                86 DVNYAFLHATDLLPACDGER 105
                                                                                          1 DVNYAFLHATDLLPACDGER 20
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                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1993; U11705.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
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02-DEC-1993; U11705.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baekkeskov S, Kim
WPI; 94-200193/24.
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WPI; 94-200193/24.
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R59524
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W34519 standard; protein; 584
W34519;
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                                                                                                                                                                                                                                                       1 DVNYAFLHATDLLPACDGER 20
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                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                       86 DVNYAFLHATDLLPACDGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1998 (first entry)
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25-NOV-1997.
02-DEC-1993; 161290.
02-DEC-1993; US-161290.
03-DEC-1992; US-984935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAEK/) BAEKKESKOV S.
(KIMJ/) KIM J.
(NAMC/) NAMCHUK M.
(RICH/) RICHTER W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GAD65 protein
stiff man syndrome
                                584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIY/) SHI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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WO9700891-A1.
                                Sequence
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Examples: Fig 1: 31pp; English.
This represents a human GAD65 protein sequence. The invention provides soluble fragments of GAD65 that are specifically reactive with at least one class of GAD65 autoantibody. The fragments are substantially free of N-terminal amino acids that would otherwise limit solubility. Different fragments contain different epitopes for different classes of GAD65 autoantibodies. These fragments are used in the methods of the invention for detection of GAD65 autoantibodies. The methods are used for diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and
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Human GAD65 protein sequence.
GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM; insulin-dependent diabetes mellitus; stiff man syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 94.200133/24.

New soluble fragments of glutamic acid decarboxylase protein - used for the diagnosis and treatment of insulin dependent diabetes mellitus and striff man syndrome.

Disclosure: Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59518-25) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for
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DB 1; Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 146; DB 1; Length 554; Best Local Similarity 100.0%; Pred. No. 4.60e-09; Matches 20; Conservative 0; Mismatches 0; Indels
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shi Y;
                                                                                                                                                                                                                                                                                                                                                                      09-NoV-1994 (first entry)
ADD65 1-31 deleted, C45A mutant.
GAD65; glutamate-decaboxylase; dlabetes mellitus; stiff man syndrome; autoantibody; mutagenesis.
                             Pred. No. 4.60e-09;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim J, Namchuk M, Richter W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               different classes of GAD65 autoantibodies
Score 146;
                                                                                                                                                                                                                                                       .T 6
R59518 standard; protein; 554 AA.
R59518;
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W86017 standard; protein; 584 AA.
                                                                                                                        86 DVNYAFLHATDLLPACDGER 105
                                                                                                                                                         1 DVNYAFLHATDLLPACDGER 20
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100.08;
                          Best Local Similarity 100.0%;
Matches 20; Conservative
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02-DEC-1993; U11705.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
Baekkeskov S, Kim J, Na
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02-DEC-1993; US-161290.
03-DEC-1992; US-984935.
25-WAY-1995; US-450755.
(REGC ) UNIV CALIFORNIA.
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WO9412529-A.
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Query Match
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Stiff-man syndrome
Disclosure; column 27-30; 30pp; English.
This sequence represents the human glutamic acid decarboxylase protein
This sequence represents the human glutamic acid decarboxylase protein
This sequence represents the human glutamic acid decarboxylase protein
This sequence represents the human glutamic of a GAD65 protein that
are specifically reactive with a GAD65 autoantibody (AAb), where the
fragment is at least 99 pure and the AAb binds to a conformational
epitope of the fragment. The soluble GAD65 fragments can be used to
distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff
man syndrome. They can also be used for diagnosts and treatment of IDDM
and stiff man syndrome. The fragments can distinguish different temporal
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W12402;
08-00T-1997 (first entry)
65 kD human glutamic acid decarboxylase isoform.
65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas; neuron; central nervous system; type I diabetes; autoimmune response; I cell; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAD65; glutamic acid decarboxylase protein; human; soluble fragment; autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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. 4.50e-09;
.... 0; Indels
                               Length 584;
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Score 146; DB 1; Length 384
Pred. No. 4.60e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y; WPI; 98-017711/02.
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ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 4.
Matches 20; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stages in the progression of IDDM. Sequence 584 AA:
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24-UON-1995; U10790.
23-UON-1995; US-49464.
(KENN-) KENNEDY INST RHEUMATOLOGY.
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Matches
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                                                                                                                                                                                    for ameliorating auto-immune responses.

Since an expression to the pance of the central nervous system. There are two bisclosure: Fig 1: 28pp; English.

This sequence represents the 65 kD isoform of human glutamic acid decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of the pancreas, and in neurons of the central nervous system. There are two considerates of the interpretation of the central nervous system. There are two GAD65 have been identified in Type I diabetic patients. Fragments of GAD65, and analogues of the fragments, are used in the methods of the invention. The methods are for detecting or treating diabetes or a predisposition to diabetes. The peptides can also be used for ameliorating an autoimmune response in a patient. Alteration of the native peptides with selective changes of crucial residues can induce the interpretation of the responsiveness of antispen specific autoreactive T cells. The peptide analogues compete for binding to MHC concerned to the corresponding native peptide seasons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                              New human glutamic acid decarboxylase peptide(s) - used for treatment, diagnosis and determining predisposition to diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders such as insulin-dependent diabetes mellitus (IDDM) and other diseases, e.g. neurological diseases, esp. in individuals having a genetic predisposition for IDDM or with an increased antibody titre against GAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified glutamic acid decarboxylase (K396R). Glutamic acid decarboxylase; of ADL; autoimmune disease; therapy; indulin-dependent diabetes mellitus; vaccine; engineering; protein engineering.
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27-SEP-1996; SE1210.
29-SEP-1995; SE-603379.
(SYNE-) SYNECTICS BIOTECHNOLOGY AB.
    Londei M;
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Pred. No. 4.60e-09;
0; Mismatches 0;
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0; Mismatches 0
Ling N,
    Leslie RDG,
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Best Local Similarity 100.0%;
Matches 20; Conservative
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Best Local Similarity 100.0%;
Matches 20; Conservative
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    Gaur A,
Conlon PJ, Gaur A
WPI; 97-087322/08.
N-PSDB; T61097.
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Disclosure; Fig 2, 45pp; English.

The sequence is that of human pancreatic islet glutamic acid decarboxylase (GAD) which is used to test biological samples for the presence of autoantibodies to human GAD. It can also be used to remove antibodies against GAD from plasma in order to treat an autoimmune response to GAD, e.g. in insulin-dependent diabetes melting (IDDM), and may also be used to induce immunological tolerance to GAD by giving GAD that specifically binds the GAD receptor on immature I
                                                                                                                                                            20-APR-1993 (first entry)
Human pancreatic islet cell glutamic acid decarboxylase.
GAD; insulin dependent diabetes melting; IDDM; autoantibody detection.
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15-MAY-1991; US-702162.
(UNIW ) UNIV WASHINGTON.
(ZIMO ) ZIMOGENETICS INC.
FOSTER DC, Grubin CE, Hagopian W, Karlsen AE, Lernmark A, OHara PJ;
N-PSDB; Q31789.
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The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acid that limit solubility. Different fragments contain epitopes fo sequence 585 AA;
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Pred. No. 4.60e-09;
0; Mismatches 0; Indels
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09-710-1994.
02-DEC-1993; U11705.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
....rov S, Kim J, Namchuk M, Richter W, Shi Y;
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Pred. No. 4.60e-09;
                                                                                                                        standard; Protein; 585 AA.
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86 DVNYAFLHATDLLPACDGER 105
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                     1 DVNYAFLHATDLLPACDGER 20
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                    LT 11
R28756 S'
R28756;
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R59516 S1
R59516;
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Homo sapiens.
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binding_site
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A modified human glutamic acid decarboxylase (GAD) (W14915) has the native Lys residue at amino acid position 36 replaced by 11e, Gln, H1s, Gly or esp. Arg (see also W14915). It is obtd. by sitedirected mutagenesis of native human GAD65 cDNA and expression of
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis and treatment of auto: immune disease, esp. insulin dependent diabetes, also related nucleic acid, vectors, antibodies, hybridoma(s) etc.

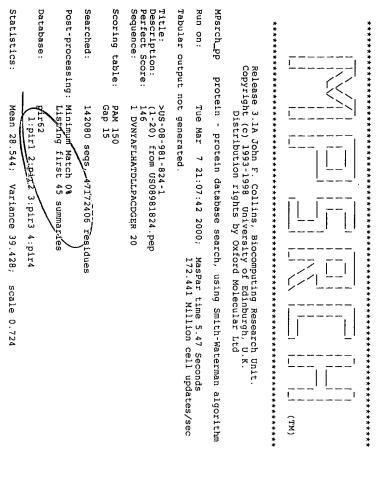
Sample 1; Fig 3; 100pp; English.

O86481 and O86482 encode R71733 and R79105, rat and human glutamic acid decarboxylase (GAD65) respectively, from which the GAD65 fragments described in R72261-R72298 were derived. These fragments can be used to detect autoantibodies against GAD, e.g. to diagnose and treat GAD-related autoimmune disorders, such as insulin dependent diabetes mellitus or stiff man disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-1997 (first entry) Modified glutamic acid decarboxylase. Glutamic acid decarboxylase. Glutamic acid decarboxylase; GAD: autoimmune disease; therapy; indulin-dependent diabetes mellitus; vaccine; enzyme englneering; protein engineering.
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Human glutamic acid decarboxylase (GAD65).
Rat glutamic acid decarboxylase; GAD65; auctimmune disorders; tansulin-dependant diabetes mellitus; stiff man disease.
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    Indels
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WPI; 95-131360/17.
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    Mismatches
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27-SEP-1996; SE1210.
29-SEP-1995; SE-003379.
(SYNE-) SYNECTICS BIOTECHNOLOGY AB.
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R79105;
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Best Local Similarity 100.0%;
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17-SEP-1993; US-123859.
(REGC ) UNIV CALIFORNIA.
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A human islet cDNA library was screened for colonies containing GAD CDNA using probes (given in 086047-49) based on conserved internal and N- and C-terminal regions of cat, rat and mouse brain GAD. Full-length clones were obtained by PCR-RACE. The entire sequence of the human islet GAD cDNA is given in 086046 and the encoded protein in R71641. GAD was used to screen sera for the presence of GAD autoantibodies.
the mutant DNA in transformed host cells. Lys-396 is critical for enzyme activity. By replacing it with an amino acid incapable of Schiff base formation, immunoreactivity is maintained but enzyme activity is reduced or lost, so minimising the risk of toxicity. The modified GAD can be used to treat and/or prevent autoimmune disorders such as insulin-dependent diabetes mellitus (IDDM) and other diseases, e.g. neurological diseases, esp. in individuals having a genetic predisposition for IDDM or with an increased antibody titre against GAD.
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non-insulin-dependent diabetes; NIDDM; diagnosis; autoantibody;
pancreas; islet.
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WPI: 95-12351
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/label= Pyridoxal-5'-phosphate_binding_site
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02-SEP-1994; U09937.
07-SEP-1993; US-117907.
(UNIW ) UNIV WASHINGTON.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result
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glutamate decarboxyla protein tyrosine-phos aldose l-epimerase (EC 4 L-serine dehydratase nudel protein precurs killer toxin kR4 prec malate synthase (EC 4 fumarate hydratase - hypothetical protein glutamate decarboxyla hypothetical narbonin probable narbonin - glutamate decarboxyla	Description
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ALIGNMENTS

RESULT 2 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS	Query Match Best Local Sim Matches 20; Db 86 DVNYAF Qy 1 DVNYAF	396 SUMMARY	#CTOSS Th	#cross-references #accession \$38! ##status ##molecule_type ##residues	ACCESSIONS REFERENCE #authors #journal #title	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE
A41292 #type complete glutamate decarboxylase (EC 4.1.1.15) 2 - human glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Homo sapiens #common_name man 18-Jun-1999 #sequence_revision 23-Mar-1995 #text_change A41935; A41292; S30058; B54778	CUETY MATCH CUETY MATCH GUETY MATCH Best Local Similarity 100.0%; Pred. No. 1.56e-19; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 86 DVNYAFLHATDLLPACDGER 105	<pre>#binding_site pyridoxal phosphate (Lys) (covalent) #status predicted #length 585 #molecular-weight 65224 #checksum 7599 .</pre>	##cross-references GB:L16980; NID:g413867; PIDN:AAA93049.1; PID:g413868 T This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. FICATION #superfamily human glutamate decarboxylase DS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate	ss-references MUID:94032481 ession	\$38533 \$38533 Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L. Biochim. Biophys. Acta (1993) 1216:157-160 Cloning and sequence analysis of a murine cDNA encoding	338533 #type complete glutamate decarboxylase (EC 4.1.1.15) 2 - mouse glutamate decarboxylase (ADA5; L-glutamate 1-carboxy-lyase #formal_name Mus musculus #common_name house mouse 20-May-1994 #sequence_revision 23-Mar-1995 #text_change

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#title Characterization of a linear epitope within the human pancreatic 64-KDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.

#cross-references.MUID:93185681
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##cross-references GB.M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
##experimental_source brain
                                                                                                                                                                                                                                                                                                                  ##cross-references GDB:128595; OMIM:138275
up_position 10p11.23-10p11.23
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NCE $30058
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86 DVNYAFLHATDLLPACDGER 105
                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ts annotation; intron-exon boundaries
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
                                             h 100.0%;
Similarity 100.0%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                stiff-man syndrome and insulin-dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karlsen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.; Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S. Grant, F.J.; Foster, D.; Lernmark, A. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341 Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bu, D.F.; Tobin, A.J.

Bu, D.F.; Tobin, A.J.

Genomics (1994) 21:222-228

The exon-intron organization of the genes (GAD1 and GAD2)

encoding two human glutamate decarboxylases (GAD-67 and

GAD-65) suggests that they derive from a common ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119 Two human glutamate decarboxylases, 65-kDa GAD an GAD, are each encoded by a single gene.
                                                                                                                                                                                                                                                                                      #superfamily human glutamate decarboxylase
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                                                                                                                                                                                                                                                                  carbon-carbon lyase; carboxy-lyase;
                                                                                                                                                                                                                                                                                                                                                                     GDB: GAD2
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                                                                                                                                              #length
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                                                                                                                                                                  #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.; Abney, C.C.; Berg, H.; Scherbaum,
Northemann, W.
                                                                                                                                           #status
n 585 #π
                                                                                                                                              #molecular-weight 65411 #checksum
                                                Pred.
0; 1
                                             Score 146; DB 1; L
Pred. No. 1.56e-19;
0; Mismatches 0;
                                                                                           Length 585,
                                                                                                                                                                                                                                                                  phosphoprotein; pyridoxal
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                                                0;
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TITLE
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COMMENT This enzyme catalyzes the conversion of glutamic acid

gamma-amino butyric acid

CLASSIFICATION #superfamily human glutamate decarboxylase
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#title
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#title
                                                                                                                     #authors Chang, Y.C.; Gottlieb, D.I.

J. Neurosci. (1988) 8:2123-2130

#title Characterization of the proteins purified with monoclonal
antibodies to glutamic acid decarboxylase.

#cross-references_MUID:88258610
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#accession JC4064
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##experimental_source brain
the authors translated the codon GAT for residue 86 as
##note
His, TCA for residue 198 as Ala, and CAG for residue
                                                                                ##status
                                                                                                                                                                                                                                                                                                                              ##THOLOGUE_CLYPE HAND
##TGEOSIQUES 11-585 ##Label ERL
##CTOSS-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204225
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##residues 1-585 ##label SUZ
                                                          ##molecule_type
                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 EVNYAFLHATDLLPACDGER 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutamate decarboxylase (EC 4.1.1.15) 2 - rat glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Rattus norvegicus #common_name Norway rat 31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change
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#formal_name Sus scrofa domestica #common_name domestic
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
                                                                                                      A60888
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Erlander, M.G.; Tillakaratne, N.; Tobin, A.J.
Neuron (1991) 7:91-100
Two genes encode distinct glut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JH0423; A60888
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Gene (1995) 152:257-260
Sequences of two porcine glutamic acid
67-kDa GAD).
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protein
'V',191194,'X',196-203,'XX',206-219;'X',225-234,'X',
236-247,'X',249-266,'X',524-537,539-543,'V',547-549
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                                                                                preliminary
                                                                                                                                                                                                                                                    His, TCA for residue 428 as Trp
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Pred. No. 2.81e-19;
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##Cross-references FlyBase:FBgn0014007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
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Local Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVNYAFLHATDLLPACDGER 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'X',551-553,'X',555-558 ##label CHA
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
TION #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily protein-tyrosine-phosphatase, receptor type
PTP69D; fibronectin type III repeat homology;
immunoglobulin homology; leukocyte common antigen cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine-phosphatase (EC 3.1.3.48), receptor typ profesp precursor - fruit fly (prosophila melanogaster) protein-tyrosine-phosphatase DPTP #formal_name Drosophila melanogaster 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain homology; protein-tyrosine-phosphatase homology
glycoprotein; phosphoprotein; phosphoric monoester hydrolase;
transmembrane protein; tyrosine-specific phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H. Proc. Natl. Acad. Sci. U.S.A. (1989) 86:8698-8702
A family of receptor-linked protein tyrosine phosphatases humans and Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B36182
A36182
#length
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#status predicted
jth 585  #molecular-weight 65402  #checksum 7756
                                  #binding_site substrate phosphate (Arg) #status
predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #product protein tyrosine-phosphatase, receptor type PTP69D #status predicted #label MATN #domain extracellular #status predicted #label EXTN #domain immunoglobulin homology #label TYTN #company #label EXTN #company #la
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#binding_site substrate phosphate (Arg) #status
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#active_site Cys (phosphocysteine intermediate) #status
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#domain immunoglobulin homology #label IM2\
#domain transmembrane #status predicted #label IMN\
#domain intracellular #status predicted #label INT\
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#molecular-weight 167410
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Pred. No. 9
2; Mismat
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. 9.76e-17;
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#checksum 8905
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Best Local
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Best Local Similarity 35.0%;
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#title
                                                                                                                                                                                                             The complete genome sequence of Escherichia coli K-12. #cross-references MUID:97426617 #accession F64942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:90299833 #accession B44509
                        #title
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                                                         #authors
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                                                                ##cresiones 1-454 ##label BLAT ##cross-references GB:AE000275; GB:U00096; NID:g1788106; ##cross-references GB:AE000275; GB:U00096; NID:g1788116; UWGP:b1814 ##experimental_source strain K-12, substrain MG1655 SUCE JV0036
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Local Similarity 57.1%;
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#length 34
Su, H.; Lang, B.F.; Newman, E.B.
J. Bacteriol. (1989) 171:5095-5102
L-serine degradation in Escherichia
sequencing of the sdaA gene.
                                                                                                                                                                                                                                                                                                    Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N. Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J. Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWECL #type complete L-serine dehydratase (EC L-serine deaminase 1
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Carbohydrate utilization in Streptococcus t
Characterization of the genes for aldose
(mutarotase) and UDPglucose 4-epimerase.
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                                                                                                                                                                                                                                                                                                                                                                                              F64942; JV0036
                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Escherichia coli
30-Jun-1991 #sequence_revision
18-Jun-1999
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                                                                                                                                                                                                  preliminary; nucleic acid
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                                                                                                                                                                                   translation not shown
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Pred. No. 1.18e+00;
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Pred. No. 4.97e-01
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                      coli K-12: cloning
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                                                                                                                                                                                                                                                                                                                        C.A.; Perna, N.T.;
J.; Glasner, J.D.;
Davis, N.W.;
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#cross-references MUID:89359152

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RESULT
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Matches 8; Conservative
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1396-1430
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title An unusual mosaic protein with a protease the nudel gene, is involved in defining dorsoventral polarity in Drosophila. #cross-references MUID:95401268 #accession A57096
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##cross-references GB:M28695
##experimental_source strain K12
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##residues 7-219,'N',221-454 ##label
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##cross-references FlyBase:FBgn0002926
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Similarity 47.1%;
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   S40034
killer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily microbial L-serine dehydratase
carbon-oxygen lyase; gluconeogenesis; hydro-lyase; lyase;
pyridoxal phosphate; serine catabolism
#length 454 #molecular-weight 48906 #checksum 2174
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#label LDL3
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#type complete
in KP4 precursor -
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Pred. No. 1.18e+00;
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Pred. No. 1.18e+00;
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Best Local Similarity 50.0%;
Matches 7; Conservative
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#title
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#accession
                 #title The complete genome
#cross-references MUID:97426617
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##molecule_type DNA
##condaines 1-533 ##label BYR2
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NCE S14734
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##residues 1-127 ##label PAR
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                                                                                   Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao
                                                                                                                                                                                                                                                         Byrne, C.R.; Stokes, H.W.; Ward, K.A.
Nucleic Acids Res. (1988) 16:10924
Nucleotide sequence of the aceB gene encoding malate synthase
A in Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                     Byrne, C. submitted to the A32649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYECMA #type complete
malate synthase (EC 4.1.3.2) A - Escherichia coli
#formal_name Escherichia coli
31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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Structure and heterologous expression
viral toxin KP4
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19-Mar-1997 #sequence_revision 19-Mar-1997 #t
13-Sep-1998
240034; S14734
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                                                       Science (1997) 277:1453-1462
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23-52 ##label GAN
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#product killer toxin KP4 #status experimental #label
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Pred. No. 1.80e+00;
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                                  sequence
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                                    of Escherichia coli K-12
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##residner
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##cross-references GB.AE0001861; GB.AE001363; NID:g4377330;
#EDN:AAD19150 1; PID:g4377343
##experimental_source strain CWL029
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PIDN:AAC76984.1; PID:g1790444; UWGP:b4014
##experimental_source strain K-12, substrain MG1655
##molecule_type
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Similarity 46.2%;
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Similarity 66.7%;
8; Conservative
                                                                                                      hypothetical protein YORO64c - yeast (Sacch cerevisiae)
hypothetical protein O2815
#formal_name Saccharomyces cerevisiae
12-Jul-1996 #sequence_revision 12-Jul-1996
14-Nov-1997
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$66929
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Olinger, L.; Grimwood, J.; Davis, R.W.; Stephens,
Nature Genet. (1999) 21:385-389
Comparative genomes of Clamydia pneumoniae and C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fumarate hydratase - Comptere (
#formal_name Chlamydia pneumoniae (
23-Apr-1999 #sequence_revision 23-Apr-1999 (
22-Jun-1999
                  submitted to the Protein S66947
                                               Bohn, C.; Bolotin
D.V.; Valens, M
                                                                                                                                                                                                                                                                                                                                                                                            #superfamily fumarate hydratase #length 460 #molecular-weight 50441 #checksum
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carbon-carbon lyase; glyoxylate bypass; oxo-acid-lyase
#length 533 #molecular-weight 60273 #checksum 1098
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translation not shown
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                                                         Bolotin-Fukuhara,
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/dratase - Chlamydia pneumoniae (strain CWL029)
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Pred. No. 1.80e+00;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                               Score 62; DB 2; I
Pred. No. 2.74e+00;
                                                                                                                                                                                                                                                                                                                                    Mismatches
                            Sequence
                                                         M.; Daignan-Fornier,
                                                                                                                                                                                       yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 533;
                                                                                                                                                                                                                                                                                                                                                                Length 460;
                            Database, July 1996
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                                                           B.;
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                                                                                                                                CLASSIFICATION KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
#authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSIONS
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Best Local Similarity 47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.

Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775

#title Developmentally regulated expression of an exon containing

#title stop codon in the gene for glutamic acid decarboxylase.

#cross-references MUID:91062362
                                                                                                                                                                                                                                                                                                                                      #description
                                                                                                                                                                                                                                                                                                                                                                    #submission
                                                                                             ##cross-references EMBL:246834; NID:9600103; PID:9600104
###experimental_source seed
FICATION #superfamily alcohol sulfotransferase
tos
seed; storage protein
#length 286 #molecular-weight 32575 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-223 ##label RES
##cross-references GB:M38350; NID:g204231; PIDN:AAA41185.1; PID:g204232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status preliminary; translated from GB/EMBL/DDBJ##molecule_type mRNA
                                                                                                                                                                                                                                 ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references EMBL:274972;
MIPS:YOR064c
                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##experimental_source strain S288C
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                             Local
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Similarity 47:1%;
                             Similarity
                                                                                                                                                                                                                                                                                                         Nong, V.; Schlesier, B.; Muentz, K. submitted to the EMBL Data Library, November 1994 The narbonin gene from Vicia faba L. $49897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I59173 #type complete
glutamate decarboxylase - rat
#formal_name Rattus norvegicus
02-Jul-1996 #sequence_revision
22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $49897 #type complete hypothetical narbonin-like 2S protein (clone pVFNA4) - bean
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#length 219
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S49897
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  41.8%;
larity 31.3%;
Conservative
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                                                                                                                                                                                                                                                                                    preliminary
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Score 61; DB Pred. No. 4.16 6; Mismatche
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5; Mismatches
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                                                  DB 2;
                          6e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #common_name Norway rat
02-Jul-1996 #text_change
                                                Length 286;
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Qy Db

129 DINYEYIKSDELFVNC 144
| | | | | : | : | : | : | |
| DVNYAFLHATDLLPAC 16

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ENTRY

ENTRY

ENTRY

Probable narbonin - jack bean
ORGANISM

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ACCESSIONS

ACCESSIONS

ACCESSIONS

ACOUNTY

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Brith and Canavalia ensiformis #common_name jack bean
DATE

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Standard and Canavalia ensiformis #common_name jack bean
DATE

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Brith and Common Canavalia ensiformis.

ACOUNTY

# accession

Standard

ACONA encoding putative narbonin from Canavalia ensiformis.

# accession

Standard

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Standard

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******************** (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Tue Mar 7 21:02:37 2000: MasPar time 3.45 Seconds 173.144 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-981-824-1 (1-20) from US08981824.pep 146

Sequence: 1 DVNYAFLHATDLLPACDGER 20

Scoring table: PAM 150 Gap 15

Searched: 82229 segs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 29.144; Variance 36.336; scale 0.802

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		. Re
18 17 19	111111 14310987654321	Result No.
59911	1466 1466 6466 6666 661	Score
41.8 41.8 40.4 40.4	100.0 100.0 99.3 99.3 92.2 43.8 43.8 43.8 41.8 41.8	Query Match
594 770 133	12	Length
	4444444444	BB
DCEL_FELCA DCEL_HUMAN YRN9_CAEEL YBB8_YEAST CLAA_LYCES	DCE2_HUMAN DCE2_MOUSE DCE2_FOI DCE2_RAT DTP6_DROME GALM_STRIR SDLL_ECOLI NDL_DROME KP4_UMV4 Y4NG_RHISN MASY_ECOLI DCE1_RAT DCE1_RAT DCE1_RAT DCE1_PIG	ID
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	61 41.8 594 1 DCEL_FELCA GLUTAMATE DECARBOXYLAS 1. 61 41.8 594 1 DCEL_HUMAN GLUTAMATE DECARBOXYLAS 1. 61 41.8 770 1 YRN9_CAEEL HYPOTHETICAL 84.2 KD p 1. 59 40.4 133 1 YBB8_YEAST HYPOTHETICAL 15.5 KD p 3. 59 40.4 926 1 CLAA_LYCES ATP-DEPENDENT CLP PROT 3.	6 100.0 585 1 DCE2_HUMAN GLUTAMATE DECARBOXYLAS 7.4 6 100.0 585 1 DCE2_BOUSE GLUTAMATE DECARBOXYLAS 7.4 5 99.3 585 1 DCE2_RAT 5 99.3 585 1 DCE2_RAT 6 LUTAMATE DECARBOXYLAS 7.4 5 92.5 585 1 DCE2_RAT 6 44.3 8 348 1 GALM_STRTR ALDOSE 1-EPIMERASE 1 3.7 4 43.8 348 1 GALM_STRTR ALDOSE 1-EPIMERASE 1 3.7 4 43.8 2616 1 NDL_DROME SERINE PROTEASE 1 3.7 4 43.8 2616 1 NDL_DROME SERINE PROTEASE 1 3.7 4 43.8 2616 1 NDL_DROME SERINE PROTEASE 1 3.7 5 43.2 12.7 1 KP4T_UMV4 KP4THICAL 42.8 KD p. 5.9 6 43.2 353 1 MASY_ECOLI MALATE SYNTHASE A (EC 1.4 6 59.3 1 DCE1_RAT GLUTAMATE DECARBOXYLAS 1.4 6 1.4 1.8 59.4 1 DCE1_RAT GLUTAMATE DECARBOXYLAS 1.4 6 1.4 1.8 59.4 1 DCE1_BIG GLUTAMATE DECARBOXYLAS 1.4 6 1.4 1.8 59.4 1 DCE1_HUMAN GLUTAMATE DECARBOXYLAS 1.4 6 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4

sera from insulin-dependent diabetes mellitus patients.";

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
55	55	56	56	56	56	56	56	57	57	57	57	57	57	57	57	57	57	57	58	58	58
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BXF_CLOBO	YO30_BPHP1	DYHC_CAEEL	CNG4_HUMAN	PLAP_RAT	PLAP_MOUSE	MUTA_PROFR	YAC3_SCHPO	YNE9_YEAST	AHR_RAT	AHR_HUMAN	PME1_CITSI	PME2_ARATH	GRBE_HUMAN	SRC_AVISR	SRC_RSVSR	SRC_RSVPA	FUMH_BACSU	YDO9_SCHPO	VIT_ACITR	CNG4_BOVIN	ALOX_CANBO
XHZ	HYPOTHETICAL 20.8 KD P	DYNEIN HEAVY CHAIN, CY	CYCLIC-NUCLEOTIDE-GATE	PHOSPHOLIPASE A-2-ACTI	PHOSPHOLIPASE A-2-ACTI	METHYLMALONYL-COA MUTA	HYPOTHETICAL 56.6 KD P	HYPOTHETICAL 98.9 KD P	AH RECEPTOR (ARYL HYDR	AH RECEPTOR (ARYL HYDR	PECTINESTERASE 1.1 PRE	PECTINESTERASE 2 (EC 3	GROWTH FACTOR RECEPTOR	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	FUMARATE HYDRATASE, CL	HYPOTHETICAL 31.5 KD P	VITELLOGENIN PRECURSOR	240 KD PROTEIN OF ROD	ALCOHOL OXIDASE (EC 1.
	1.93e+01		1.27e+01	1.27e+01	1.27e+01	1.27e+01	1.27e+01		8.36e+00	8.36e+00	8.36e+00	8.36e+00	8.35e+00	8.36e+00	8.36e+00	8.36e+00	8.36e+00	8.36e+00		٠.	٠.

ALIGNMENTS

CE	STANDARD; PRT;	585 AA.
01-FER-1996	(Rel. 33.	
01-FEB-1996	(Rel. 33, Last	update)
01-FEB-1996	48	te)
PAM	σ)RM (EC 4.1.1.15) (GAD-65)
G	AMIC ACID DECARBOXYLASE)	
0	65.	
Homo sapiens	Ċ	
Eukaryota; 1	Chordata; Cr	ita; Vertebrata; Mammalia;
Eutheria; Pi	Catarrhini;	Hominidae; Homo.
Ξ		
	OM N.A.	
	196068.	
BU DF., EI	., HITZ	TILLAKARATNE N.J., KAUFMAN D.L.,
WAGNER-MCPHI	ERSON C.B., EVANS G.A., T	
"Two human o	glutamate decarboxylases	65-kDa GAD and 67-kDa GAD, are
each encoded	d by a single gene.";	
Proc. Natl.	Acad. Sci. U.S.A. 89:21:	89:2115-2119(1992).
[2]		
	OM N.A.	
MEDLINE; 94	375018.	
"The exon-in	etron organization of the	genes (GAD1 and GAD2) encoding
two human g	lutamate decarboxylases	and GAD65) sugges
they derive	from a common ancestral	;
Genomics 21	:222-228(1994)	
SEQUENCE FRO	٠	
TISSUE-PANCI	REATIC ISLETS;	
MEDLINE; 920		
KARLSEN A.E	., HAGOPIAN W.A., GRUBIN	.E., DUBE S.,
ADLER D.A.,	BARMEIER H., MATHEWES S	GRANT F.
LERNMARK A.		
	d primary structure of a	human islet isoform of glutamic
	oxylase from chromosome	
	Acad. Sci. U.S.A.	5/-8341(1991).
		•
SEQUENCE OF	6-585 FROM N.A.	
TISSUE-PANCI	REAS;	
MEDLINE; 93:	185681.	
MAUCH L., AI	Y C.C., BERG H.,	SCHERBAUM W.A., LIEDVOGEL B.,
NORTHEMANN V		
"Characteria		n pancreatic
64-KDa giuta	5	ind its autoimmune recognition by
	RESULT 1 DCE2_HMAN AC Q05329; DT 01-FEB-1996 C 65 KD TEB-1996 C 65 KD TEB-1996 C C Utheria; P. RN MEDLINE; 92 RA WEDLINE; 92 RA WEDLINE; 94 RT each encodes RL Proc. Nat1. RY SEQUENCE FR RY MEDLINE; 94 RY MEDLINE; 94 RY MEDLINE; 94 RY MEDLINE; 94 RY T'TWO human 9 RY T'TO HUMAN 1 RY SEQUENCE FR RY MEDLINE; 94 RY SEQUENCE FR RY MEDLINE; 92 RA KARLSEN A.E RA LERNMARK A. RY "Cloning an acid decarbing an acid decarbin	OS329; OS329; I-FEB-1996 (Rel. 33, Created) I-FEB-1996 (Rel. 33, Last seq I-FEB-1996 (Rel. 32, L

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Best Local :
                                                                                                                                                                                                                                                                                                                                                      P48320: 035519;
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81882; AAA62367.1; -.
EMBL; M74826; AAA59491.1; -.
EMBL; K9936; CAA49554.1; ALT_INIT.
EMBL; M70435; AAA52513.1; -.
PIR; A41292; A41292.
PIR; PQ0158; PQ0158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                         ASADA H., KAWAMURA Y., MARUYAMA K., KUME H., DING R. KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.; "Mice lacking the 65 kDa isoform of glutamic acid de (GAD65) maintain normal levels of GAD67 and GABA in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
                                                                                                                              STRAIN=C57BL/6; TISSUE=BRAIN; MEDLINE; 97115675.
                                                                                                                                                                                                                                     STRAIN=C57BL/6; TI
MEDLINE; 94032481.
                                                                                                                                                                                                                                                                                                                                                                                                                         DCE2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyridoxal phosphate;
BINDING 396 3:
             TISSUE-BRAIN
                        SEQUENCE OF 175-379
                                                                 are susceptible to seizures.";
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                               "Cloning and sequence analysis decarboxylase (GAD65).";
                                                                                                                                                                                                                         LEE D.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                              65 KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y Match 100.0%;
Local Similarity 100.0%;
nes 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE +

COFACTOR: PYRIDOXAL PHOSPHATE.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                OR GAD65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biochem. 212:597-603(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVNYAFLHATDLLPACDGER
                                                                                                                                                                                                                       .S., TIAN
                                                                                                                                                                                                                                                                                                                                             GLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00392; DDC_GAD_HDC_YDC;
                                               Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                          Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 AA;
                                                                                                                                                                                                                         J., PHAN T.,
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                  Acta 1216:157-160(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 P
65411 MW;
                        FROM N.A
                                                                                                                                                                                                                                                                                       Chordata; Craniata; Ver
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                             DECARBOXYLASE).
                                                                                                                                                                                                                         KAUFMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 146; DB 1;
Pred. No. 7.49e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRIDOXĀL PHOSPHATE ; 8AD62B62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                           of a murine
                                                  229:891-895(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                       D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                          585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                         Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                       4.1.1.15) (GAD-65)
                                                                                                                                                                                                            CDNA
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                                                                                                    . R.G.,
                                                                                       decarboxylase
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                                                                                                                                                                                                                                                                                         Mammalia;
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                                                                            their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                  JI F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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Best Local S
Matches 2
                                                SUZUKI R., ASAMI N., AMANN E., WAGATSUMA "Sequences of two porcine glutamic acid d 67-kDa GAD).", Gene 152:257-260(1995).

-!- FUNCTION: CATALYZES THE PRODUCTION OF -!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-A.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWI
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                         DCE2_PIG STANDARD; PRT; 58
P48321;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence upd
01-FEB-1996 (Rel. 33, Last annotation upd
01-FEB-1996 CRED. 55 KD ISSPORM
(65 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L16980; AAA93049.1; -. EMBL; D42051; BAA22893.1; -. EMBL; S67454; CAB32806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Localization and quantitation of expression of two glu decarboxylase genes in pancreatic beta-cells and other tissues of mouse and rat.",
Endocrinology 133:2962-2972(1993).
-!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYZIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE
-!- COTALTIC ACTIVITY: B-GLUTAMATE.
                                                                                                                                                                                                                                                               GAD2 OR GAD65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurotransmitter
Pyridoxal phospha
BINDING 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See or send an email to license@isb.sib.ch).
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:95634; GADZ.
PROSITE; PS00392; DDC_GAD_HDC_YDC;
                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
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                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collal een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%, 20; Conservative
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                                                                                                                                                                     95137399
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259 25
319 319
319 31
325 32
499 49
585 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyridoxal_deC; 1.
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ate; Multigene family
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                                                                                                                                          N E., WAGATSUMA M.; glutamic acid deca
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Pred. No. 7.49e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE (POTENTIAL).

F -> S (IN REF. 2).

I -> S (IN REF. 3).

K -> E (IN REF. 2).

P -> S (IN REF. 2).

; 9BE5C088 CRC32;
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                                                    DECARBOXYLASES
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                                                                                                                                                                                                                                                                                      update)
                                                                                          4 - AMINOBUTANOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Decarboxylase;
                                                                                                       OF GABA
                                                                                                                                             decarboxylases
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                                                                                          + co(2)
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                                                                                                                          Query Match
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                                                                                                                                                                                               PROSITE; PS00392; DOC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxyla
Pyridoxal phosphate; Multigene family.
BINDING 396 9YRIDOXAL PHOSPHATE
SEQUENCE 585 AA; 65402 MW; E35D601A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOBIN A.J.;

"Two genes encode distinct glutamate decarboxylas

"Two genes encode distinct glutamate decarboxylas

"Legrand 7:91-100(1991).

"I FUNCTION: CATALYZES THE PRODUCTION OF GABA.

"I CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTA

"I COFACTOR: PYRIDOXAL PHOSPHATE.

"I SUBUNIT: HOMODIMER (BY SIMILARITY).

"I SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCE2_RAT STANDARD; PRT; 585 AA.
Q05683;
Q1-FEB-1996 (Rel. 33, Created)
Q1-FEB-1996 (Rel. 33, Last sequence update)
Q1-FEB-1996 (Rel. 33, Last annotation update)
G1-FEB-1996 (Rel. 33, Last SCPORM (EC 4.:
G5 KD GLUTAMATE ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-HIPPOCAMPUS;
MEDLINE; 91299343.
MERLANDER M.G., TILLAKARATNE N.J., FELDBLUM S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Peurotransmitter biosynthesis; Lyase; De
Pyridoxal phosphate; Multigene family.
BINDING 396 PYRIDOXAL P
SEQUENCE 585 AA; 65388 MW; F3E9BD88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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  DVNYAFLHATDLLPACDGER
                                               DVNYALLHATDLLPACEGER
                                                                                                                                                                                                                                                                                                                                 M72422; AAA63488.1; -. TE; PS00392; DDC_GAD_HI
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19; Conservative
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larity 90.0%;
Conservative
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Sciurognathi;
20
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Pred. No. 1.44e-21;
1; Mismatches 0;
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Pred. No. 8.98e-19;
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                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            decarboxylases.";
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Rattus.
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PFAM; PFO0047; ig; 2.

PFAM; PF00047; ig; 2.

PFAM; PF00102; Y_Dhosphatase; 2.

W Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;

Cell adhesion; Immunoglobulin domain; Duplication.

T GINAL

1 23

PROTEIN-TYROSINE PHOSPHATASE DP7

TANNSHEM 806

R23 PROTEIN-TYROSINE PHOSPHATASE DP7

DOMAIN

14 22 I422

TOMAIN

15 I5 IFBRONECTIN TYPE DOMAIN.

DOMAIN

16 I42 CYTOPLASMIC (POTENTIAL).

TOMAIN

17 DOMAIN

18 19 IG-LIKE C2-TYPE DOMAIN.

DOMAIN

19 IG-LIKE C2-TYPE DOMAIN.

TOMAIN

10 143 538

FIBRONECTIN TYPE-III.

DOMAIN

115 PROTEIN-TYROSINE PHOSPHATASE.

TOMAIN

100MAIN

115 PROTEIN-TYROSINE PHOSPHATASE.

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115 PROTEIN-TYROSINE PHOSPHATASE.

TOMAIN

1208

1459 PROTEIN-TYROSINE PHOSPHATASE.

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DISULFID

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144

POTENTIAL.

T CARBOHYD

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TO CARBOHYD

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TO CARBOHYD

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CARBOHYD

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TO CARBOHYD

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TO CARBOHYD

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TO CARBOHYD

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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DPTP PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIXEASE; FB9n0014007; Ptp66D:
PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: M27699; AAA28842.1;
PIR: B36182; B36182.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Drosophila.";
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREULI M., KRUEGER N.X., TSAI A.Y.M., SAITO H.; "A family of receptor-linked protein tyrosine phosphatases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Dipter; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYROSINE-PHOSPHATE PHOSPHOHYDROLASE) PTP69D OR'DPTP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Natî. Acad. Sci. U.S.A. 86:8698-8702(1989).
FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RE
CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O -
PROTEIN TYROSINE + ORTHOPHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (
LIKE DOMAINS FOLLOWED BY 2 FIBRONECTIN TYPE III-LIKE DOM
AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN-TYROSINE PHOSPHATASE DPTP. EXTRACELLULAR (POTENTIAL).
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CARBOHYD
                                                                                                                                                                                                                                                                      POOLMAN B., ROYER T.J., MAINZER S.E., SCHMIDT B.F.;

"Carbobydrate utilization in Streptococcus thermophilus:
characterization of the genes for aldose 1-epimerase (mutaro)
UDpglucose 4-epimerase.";
J. Bacteriol. 172:4037-4047(1990)

-i - CAPALYTIC ACTIVITY: ALPHA-D-GLUCOSE - BETA-D-GLUCOSE (ALG.
ACTS ON L-ARABINOSE, D-XYLOSE, D-GALACTOSE, MALTOSE AND 1-
-i- PATHWAY: GALACTOSE METABOLISM (LELOIR PATHWAY).

-i- SIMILARITY: TO OTHER MUTAROTASES PROTEINS AND DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P21955;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequ
01-NOV-1995 (Rel. 32, Last anno
ALDOSE 1-EPIMERASE (EC 5.1.3.3
                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                             PROSITE; PS00545; ALDOSE_1_EPIMERASE; PFAM; PF01263; Aldose_epim; 1. Isomerase; Galactose_metabolism.
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                                                                                                      Isomerase;
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
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                      221 ETNYDERKTTDLLP
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B44509; B44509
  DVNYAFLHATDLLP
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                                                                                           180
348 AA;
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(Rel. 32, Last annotation updat
IMERASE (EC 5.1.3.3) (MUTAROTASE
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209
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288
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429
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701
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larity 57.1%;
Conservative
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                                           Pred.
2; M
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Pred. No. 1.46e-01
                                                                   Score 64;
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POTENTIAL.
POTENTIAL.
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W; 881D14A4
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                                                                                            8A00D52A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tation update) (MUTAROTASE).
                                               Mismatches
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                                                        No. 3
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3.72e-01
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                                                                   Length 348
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A ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T.,
A ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M.,
A MAKINO K., MAIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
A NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
A SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H.,
A SAITO N., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.;
A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
DNA Res. 3:379-392(1996).
C-:- FUNCTION: DEAMINATES ALSO THREONINE, PARTICULARLY WHEN IT IS
CC --- FUNCTION: DEAMINATES ALSO THREONINE, PARTICULARLY WHEN IT IS
CC --- CATALYTIC ACTIVITY: L.-SERINE + H(2)O = PYRUVATE + NH(3) + H(2)O.
--- COFACTOR: IRON-SULFUR (4FE-4S) (PROBABLE).
CC --- PATHWAY: GLUCONEOGENESIS FROM SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P16095;
01-APR-1990 (Rel. 14, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1-SERINE DEHYDRATASE 1 (EC 4.2.1.13) (L-SERINE DEAMINASE 1) (SDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97426617.

BLASTMER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the sdaA gene.";
J. Bacteriol. 171:5095-5102(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SU H., LANG B.F., NEWMAN "L-serine degradation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDHL
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deaminase 1 from Escheri
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                                                                                                                        RADICAL ACTIVATION MECHANISM.
SIMILARITY: BELONGS TO THE IRON-SULFUR DEPENDENT L-SERINE DEHYDRATASE FAMILY.
                                                                                                                                                                             PTM: IT IS MADE BY THE CELL IN AN INACTIVE FORM, SUBJECT TO POST-
TRANSLATIONAL ACTIVATION BY A SYSTEM INVOLVING AT LEAST THREE GENE
PRODUCTS. THIS UNKNOWN IN VIVO SYSTEM IS MIMICKED IN VITRO BY IRON
AND DITHIOTHREITOL. THERE IS CONSIDERABLE EVIDENCE FOR A FREE-
                                                                                                                                                                                                                                                                     INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence 
nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97251358.
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Escherichia
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Cell 82:785-70...
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Matches
   EMBL: U29153; AAA83086.1;

HSSP; P00763; 1DPO.

FLYBASE: FB9n0002926; ndl.

PROSITE: PS00134; TRYPSIN_BER; 1.

PROSITE: PS00135; TRYPSIN_SER; 1.

PROSITE: PS00135; TRYPSIN_1: 6.

PROM: PF00087; ldl_recept_a; 8.

PFAM: PF00087; ldl_recept_a; 8.

PFAM: PF00089; trypsin; 1.

Serine protease: Glycoprotein: Signal; Develous PROTEASE; Repeat; 2ymogen; Extracellular mat SIGNAL 1 4 2616

CHAIN 4 2616 WIID 1.
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P98159;

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SERINE PROTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M28695; AAA63580.1; -.
EMBL; D4000275; AAC74884.1; -.
EMBL; D400275; CAB21547.1; -.
EMBL; D40025; CAB21547.1; -.
PIR; J40036; DWECL.
ECOGENE; EG10930; SDAA.
Lyase; Iron-sulfur; 4Fe-4S; Gluconeogenesis; Multigene family.
SEQUENCE 454 AA; 48906 MW; D5F3B006 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-OREGON-R; TISSUE-OVARY;
MEDLINE; 95401268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                           FUNCTION: NUDEL, PIPE AND WINDBEUTEL TOGETHER TRIGGER THE PROTEASE CASCADE WITHIN THE EXTRAEMBRYONIC PERIVITELLINE COMPARTMENT WHICH INDUCES DORSOVENTRAL POLARITY OF THE DROSOPHILA EMBRYO. NUDEL IS DIRECTLY INVOLVED IN LOCALLY PRODUCING THE TOLL LIGAND.

SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

TISSUE SPECIFICITY: FOLLICLE.

PIM: REQUITES CLEAVAGE FOR ACTIVATION (PRESUMABLY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
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82:785-794(1995).
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VNYAFLHATDLLPACD
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-1996 (Rel. 34, Last sequence update)
-1997 (Rel. 35, Last annotation update)
PROTEASE NUDEL PRECURSOR (EC 3.4.21.-).
                                                                                                                                                                                                           s requires a license agreement (See http://www.isb-sib.ch/a an email to licenseeisb-sib.ch).
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Similarity 50.0%;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with a protease domain, encoded defining embryonic dorsoventral
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Pred. No. 3.72e-01;
4; Mismatches 4
       POTENTIAL.
SERINE PROTEASE NUDEL
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                                                 Developmental protein; lar matrix.
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                                                                                                                                                                                                                                                                                                                                                                            STRAIN-M2B;
GU F., KHIM
                                                                                              between
the Euro
                                                                                                                                                                                         GU F., KHIMANI A., RANE S.G., FLURKEY W.H., BOZARTH R.F., SMITH T.J. "Structure and function of a virally encoded fungal toxin from Ustilago maydis: a fungal and mammalian Ca2+ channel inhibitor."; Structure 3:805-814(1995).

-i- FUNCTION: THIS PROTEIN IS LETHAL TO SENSITIVE CELLS OF THE SAME RELATED SPECIES. IT SPECIFICALLY INHIBITS VOLTAGE-GATED CALCIUM CHANNELS. KILLS TARGET FUNGAL CELLS BY BLOCKING DIVALENT CATION CHANNELS (VIA CALCIUM AND/OR MAGNESIUM CHANNELS).
                 EMBL; L12226; AAA89185.1;
EMBL; U25179; AAA75041.1;
PDB; 1KPT; 31-OCT-95.
                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 "OSANESA C., FLURKEY W.H., RANDHAWA Z.I., BOZARTH R.F.;
"UStilago maydis virus P4 killer toxin: characterization,
amino terminus sequence, and evidence for glycosylation."
Arch. Biochem. Biophys. 286:195-200(1991).
                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION, MEDLINE; 91378288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ustilago
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                                                                                                                  This
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                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and heterologous toxin KP4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARK C.-M., BRUENN J.A.,
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15-JUL-1998 (Rel.
15-DEC-1998 (Rel.
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                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                               SUBCELLULAR LOCATION: SECRETED.
MASS SPECTROMETRY: MW=11045; MW_ERR=11; METHOD=MALDI;
                                                                                                                                                                                  SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
_UMV4
         Signal;
                                                                                                                                                                                                                                                                                                                                                                    KHIMANI A.K.,
Led (SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 47.1%;
8; Conservative
                                                                          non-profit institutions as long and this statement is not removed.
                                                                                                                                   TO BE THE CASE ACCORDING
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dsRNA viruses; Totiviridae; Totivirus
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3D-structure
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36,
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to the EMBL/G
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3.72e-01
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P55579;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  Rhizobium sp. (strain NGR:
Plasmid sym pNGR234a.
Bacteria; Proteobacteria;
                                                                                   Hypothetical SEQUENCE 39
                                                                                                      EMBL; AE000087; AAB91786.1; -. PFAM; PF01370; Epimerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    Y4NG
                                                                                                                                                                                                                                                                               Nature 387:394-401(1997)
                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between
                                                                                                                                                                                                                                                                                                    PERRET X
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                                                                                                                                                                                                                                                                                                                                                        Rhizobiaceae;
                    243
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Pred. No. 5.
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4.2.1.46) AND NAD(P)-DEPI
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BYRNE C.R., STOKES H.W.

"Nucleotide sequence of the seque
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01-NOV-1988 (Rel. (
15-DEC-1999 (Rel. )
MALATE SYNTHASE A
                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                              DCE1_MOUSE STANDARD; PRT; 593 AA P48318; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) CRC DECARBOXYLASE, 67 KD ISOFORM (EC. 167 KD GLUTAMATE ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOGENE; EG10023; ACEB.

PROSITE; PS00510; MALATE_SYNTHASE; 1.

PFAM; PF01274; Malate_Synthase; 1.

Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.

SEQUENCE 533 AA; 60273 MW; CB05B9F8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of the Escherichia coli genome. "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
-!- CATALYTIC ACTIVITY: L-MALATE + COA - /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X12431; CAA30973.1; -.
EMBL; U00006; AAC43108.1; -.
EMBL; AE000474; AAC76984.1; -
PIR; Q00592; SYECMA.
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Bacteria; Proteobacteria;
  SEQUENCE
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PATHWAY: SE
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TRICARBOXYLIC ACID CYCLE (IN BACTERIA, FUNGI AND I
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE MALATE SYNTHASE FAMILY
                                                                                                                KD GLUTAMIC
1 OR GAD67.
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4.1.3.2) (MSA).
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Pred. No.
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                                                                                                                                                 DCE1_RAT STANDARD; PRT; 593 AA.

P18088; 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
GLUTAMATC ACID DECARBOXYLASE).
SEQUENCE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUP-BRAIN;
KATAROVA Z., SZABO G., MUGNAINI E
KATAROVA Z., SZABO G., MUGNAINI E
"Molecular identification of the
decarboxylase from the mouse.";
Eur. J. Neurosci. 2:190-202(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z49976; CAA90277.1;
EMBL; S67453; CAB32805.1;
MGD; MGI:95632; GAD1.
PROSITE; PS00392; DDC_GAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissues of mouse and rat.".

Endocrinology 133:2962-2972(1993).

FOUNCTION: CATALYZES THE PRODUCTION

CATALYTIC ACTIVITY: L-GLUTAMATE - 4

COFACTOR: PYRIDOXAL PHOSPHATE.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SIMILARITY: BELONGS TO GROUP II DEC
                      Brain
[2]
                                                                                                                                              GAD1
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                                            decarboxylase.";
                                                                                                             Eutheria;
                                                                                                                        Eukaryota;
                                                                                                                                  Rattus norvegicus (Rat).
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Local (
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                                                                                                                                              OR GAD67
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9; Conservative
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90132703.
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PS00392; DDC_GAD_HDC_YDC; 1.
                                                                                                            ; Metazoa;
Rodentia;
                                Mol. Brain
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                                                    ND R.W.,
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47.4%;
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                                Res.
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No. 1.46e+00;
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                                                                                                                                                                                                                                                        LT 14
DCE1_PIG
P48319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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BINDING
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                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
(67 KD GLUTAMATC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M34445; AAC42037.1;
EMBL; X57572; CAA40800.1;
EMBL; X57573; CAA40801.1;
EMBL; M76177; AAA41184.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. use by non-profit institutions as lo modified and this statement is not remo
                    MEDLINE; 95137399
                                                        SEQUENCE FROM N.A.
                                                                                            Eutheria;
                                                                                                           Eukaryota; Metazoa;
                                                                                                                               Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A41367; A41367
PIR; A43756; A43756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADSEN O.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICHELSEN B.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Neurochem.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, characterization, and autoimmune recognition
                                       SSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYRDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                     ETDFSNLFAQDLLPAKNGE: ::: | | | | | | | | | |
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                                                                                                                                                OR GAD67
                                                                                                                                                                                                                                                                                                                                                  DVNYAFLHATDLLPACDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TE; PS00392; DDC_GAD_HDC_YDC; PF00282; Pyridoxal_deC; 1.
 R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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                                                                                            Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphate;
                                                                                                                               (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., SAMAMA P., MALLET glutamic acid decark
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Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54:703-705(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BELONGS TO GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PETERSEN J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis; Lyase; Decarboxylase;
ate; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
284
288
345
347
380
                                                                                        Chordata; Cran
actyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                      41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           institutions as long as
   AMANN
                                                                                                                                                                                                                                                                                                                                                                                    : 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copyright. It is produced through tute of Bioinformatics and the EN.ics Institute. There are no restitututions as long as its content
                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  decarboxylase
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AG -> EA (IN REF. 2).
T -> I (IN REF. 2).
FD -> LE (IN REF. 2).
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Pred.
5; M
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F -> S (IN REF. 2).
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                                                                                                           Craniata;
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> R (IN 5A0B67C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOEL
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   WAGATSUMA
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                            Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      61; DB 1; I
No. 1.46e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EA (1.
I (IN REF. 2).
LE (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DECARBOXYLASES
                                                                                                                                                                                                                                                                          594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 - AMINOBUTANOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                           Vertebrata;
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                                                                                                                                                                                                                                                                          AA
                                                                                            Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nition of rat islet
diabetes mellitus.";
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DDC,
                                                                                                              Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYRBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
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Best Local S
Matches
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P14748;
01-APR-1990 (Rel. 14, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
61UTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4:1.1.15)
(67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O/-KUA GAD).";

Gene 152:257-260(1995).

-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

-i- CATALYTIC ACTIVITY: L-GLUTAMATE. = 4-AMINOBUTANO

-i- COFACTOR: PYRIDOXAL PHOSPHATE.

-i- SUBUNIT: HOMODIMER (BY SIMILARITY).

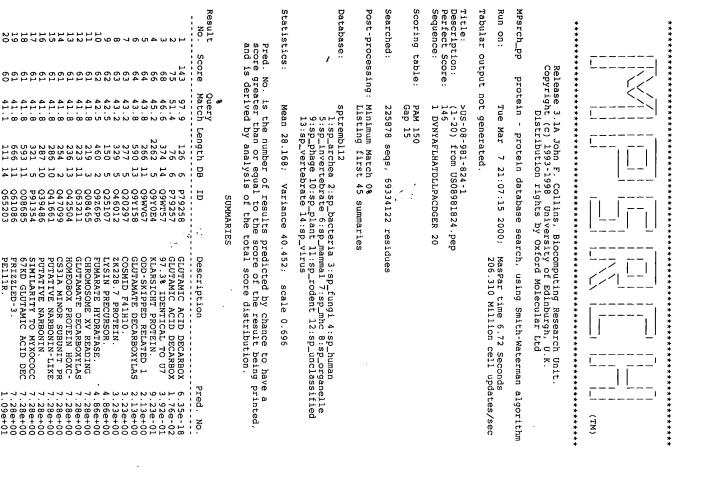
-i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                     enzymatically active fusion protein.",
J. Neurosci. 7:2768-2772(1987).
-i- FUNCTION: CATALYZES THE PRODUCTION
-i- CATALYTIC ACTIVITY: L-GLUTAMATE = 4
-i- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis Silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; De
Pyridoxal phosphate; Multigene family.
BINDING 405 PYRIDOXAL F
SEQUENCE 594 AA; 66894 MW; 69D6C79C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          EMBL; M18629; AAA51430.1; PIR; A45671; A45671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAD1 OR GAD67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J., "Glutamic acid decarboxylase cDNA: nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 87310623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=OCCIPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORTEX;
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5; M
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                                                                                                                                                                                                                                                                                                                                          DECARBOXYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; I
1.46e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                  N OF GABA.
4-AMINOBUTANOATE
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                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHATE (POTENTIAL).
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DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; pyridoxal_deC; 1.
KW Neurotransmitter blosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;
Query Match 41.8%; Score 61. DB 1; Length 594;
Best Local Similarity 47.4%; Pred. No. 1.46e+00;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
LD 92 ETDFSNLFARDLLPAKNGE 110
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ALIGNMENTS

008685 Q61086 Q65203

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Q9Y0E4;
01-NOV-1999
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
97.3% IDENTICAL TO U7 GENE (
SEQUENCE FROM N.A.

MOSLEY BISHOP K.L., LI Q., PATTERSON K., FISCHER Submitted (JUN-1999) to the EMBL/GenBank/DDBJ dat EMBL; AF157066; AAD43129.1; -.

SEQUENCE 2262 AA; 245116 MW; E35504F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 variant A and B.";
J. Virol. 0:0-0(1999).
EMBL; AB021506; BAA78227.1; -.
SEQUENCE 374 AA; 43081 MW;
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MEDLINE; 96256692.
MITSUSHIMA D., MARZBAN F., LUCHANSKY L.L., B
DURNING M., GOLOS T.G., TERASAWA E.;
"Role of glutamic acid decarboxylase in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca.
                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                            KLARSICHT
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Viruses; dsDNA viruses,
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BL; S82650; AAB46786.1; -.
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Q9WVG7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; (
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Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Chordata; Craniata; Wuridae; Murinae;
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PROSITE; PS00392; DDC_GAD_HDC_YDC;
Lyase; Decarboxylase; Pyridoxal ph
                                                                                                                                                                                                                                                                                                                                                  "Characterization of glutamate decarboxylase in chicken submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC.
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RELATED 1 PROTEIN.
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9.23e-01;
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                     SEQUENCE FROM MEDLINE; 9415 WILSON R., AI BONFIELD J.,
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BONFIELD J., BURTON J., CONNELL M., COPSEY J., COOLSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAIREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOFRA A., SAUNDERS D., SHOWNKEEN
SWALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHANK P.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M D of contiguous nucleotide sequence from chromosome III of C.
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BASHAM V.
                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
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01-JUN-1998 (TrEMBLrel.
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Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
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BLANCHARD M., BRADSHAW
Submitted (JUL-1996) to
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STRAIN-BRISTOL N2;
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MEDLINE; 94150718.
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R., AINSCOUGH R., F
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61954; AAB03172.1; -...

2024 MW;
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oidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
SIGNAL
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Q25107;
KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., (GRIMWOOD J., DAVIS R.W., STEPHENS R.S.; "Comparative Genomes of Chlamydia pneumoniae and C. trac Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEE Y.H., VACQUIER V.D.;
Submitted (NOV-1994) to the
EMBL; L26276; AAA21522.1; -.
HSSP; P04552; 1LYN.
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Haliotidae; Haliotis.
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Nature 368:32-38(1994)
                                                                                                                             STRAIN-CWL029;
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                                                                                                                                                               EQUENCE FROM N.A.
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01-NOV-1996
SEQUENCE FROM N.A.

MEDLINE; 91062362.

BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;

BOND ROM, WYBORSKI R.J., GOTTLIEB D.I.;

TOCOL NATI. Acad. Sci. U.S.A. 87:8771-8775(1990).

EMBL; M38350; AAA41185.1; -.
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Q63211;
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VALENS M.
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EMBL; Z74972; CAA99257.1; -...
EMBL; Z70678; CAA94549.1; -...
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HSSP; P05042; 1FUO.
PROSITE; PS00163; FUMARATE_LYASES;
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01-NOV-1998 (TremBLrel.
GLUTAMATE DECARBOXYLASE.
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Q08465; 000025;
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                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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ENCE 219
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                                                                                                                                                                                                                                               Rodentia;
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47.1%;
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Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
25350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50441 MW;
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Pred.
4; M
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Last annotation updat
ORF YORO64C.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1119F5E2 CRC32;
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nt of yeast chromosome X
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No. 7.
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No. 4.86e+00
                                                                                                                                                                                                                                            Muridae;
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7.28e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DANG
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                                                                                                                                                                                                                                                                          Mammalia;
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RESULT 13

ID 042504;
AC 042504;
AC 042504;
AC 042504;
AC 01-JAN-1998 (
DT 01-JAN-1998 (
DT 01-WV-1999 (
DE HOMEOBOX PROI
GENEROY-6.
OS Fugu rubripes
OC ELKARYOCIS;
MC TETRAOGONTIFC
RO TETRAOGONTIFC
RN SEQUENCE FROM
RX MEDLINE; 9728
RA APARICIO S.,
RA CHEN E., KRHI
RI "Organizatiot
RI "Organizatiot
RI CONTINUING enet."
CC -!- SUBCELLUI
DR MBL; U92572
DR HSSP; D02833
DR HSSP; P00833
DR PROSITE; PS00
DR PEAM; PF0004
DR PEAM; PF0004
DR PEAM; PROOD
DR PRINTS; PR00
DR PEAM; PROOD
DR PEAM; PEOOD
DR PEAM; PROOD
DR SEQUENCE 2
                                                                                                                                                                              RESULT 14
ID Q47099;
AC Q47099;
DT 01-NOV-1996
DT 01-NOV-1996
DT 01-NOV-1996
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  Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches
                        Signal.
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EMBL; U92572; AAB68682.1;
HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Carnitata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00282; SEQUENCE 223
                                                          DER VARTANIAN M.;
Submitted (SEP-1993)
                                                                                                                      Bacteria; P:
Escherichia
                                                                                                                                                                    CS31A MINOR
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00025; ANTENNAPEDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Organization of the Fugu rubripes continuing evolution of vertebrate Nat. Genet. 16:79-83(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97285126.
APARICIO S., HAWKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMEOBOX PROTEIN
  SEQUENCE
            CHAIN
                                                EMBL;
                                                                                    STRAIN=K-
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                              Escherichia
                                                                                                                                                           CLPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN E., KRUMLAUF R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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nes 9; Conse
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|FLHATDLLPAC
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                                                                                                                                                                                                                                                                                                                                                                                                                         PF00046; homeobox;
                                               L05182;
                                                                                                                                                                                                                                                                                                                            Similarity 6; Conser
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                                                                                                                                 Proteobacteria;
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3 (TrEMBLrel. ()
4 (TrEMBLrel. )
6 (TrEMBLrel. )
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(TrEMBLrel.
SUBUNIT PREC
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larity 47.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                AAA23586.
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AA; 25069 MW;
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 254
27021
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54.5%;
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Last seq
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Pred.
5; M
POTENTIAL.
CS31A MINOR
6B28C6FD C
                                                                                                                                                                                 Last sequence update)
Last annotation updat
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Last annotation updat
                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                      Created)
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C7162AC1 CRC32;
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7.28e+00;
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7.28e+00;
7.2° 2;
                                                                                                                                                                                                                                254
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 R SUBUNIT
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                                                                                                                                                                               update)
                                                           databases
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RESULT 15

ID Q44561
AC Q41661;
AC Q41661;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PUTATIVE NARBONIN-LIKE 2S PROTEIN.

OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC vicia.

RN [1]
RP SEOUENCE FROM N.A.
RI SUBMITTEDON;
RA NONG V. SCHLESIER B., MUENTZ K.;
RA NONG V., SCHLESIER B., MUENTZ K.;
EMBL; Z46834; CAA866975.1; -.
DR MENDEL; 16614; Vicia; 2552;16614.
DR PRINTS; PRO0551; 2SGLOBULIN.
SQ SEQUENCE 286 AA; 32575 MW; ABE3A19D CRC32;
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Job time : 11 secs.
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Best Local Similarity 31.3%;
Matches 5; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
TISSUE=COTYLEDON;
NONG V., SCHLESIER B., MUENTZ K.;
NONG V., SCHLESIER B., MUENTZ K.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; 246834; CAA68675.1; -
EMBL; 16614; Vicfa;2552;16614.
PRINTS; PRO0551; 28GLOBULIN.
PRINTS; PRO0551; 28GLOBULIN.
TOTIONCE 286 AA; 32575 MW; ABE3A19D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 DINYEYIKSDELFVNC 144
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|| |: |||:|
6 FLHATDLLPAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| :: :|: |
1 DVNYAFLHATDLLPAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 21:07:26 2000
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Pred. No. 7.28e+00;
2; Mismatches 2; Indels
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				SUMMARLES			
esult No.	Score	Query Match	Length DB	ID	ption	Pred. No.	
ш	159	100.0	20 1	W01794	Human 65 kD glutamine	5.66e-09	
2	159	100.0	20 1	W18843	65 kD Glutamic acid de	.66e-0	
w	159	100.0	341 1	R59522)65 1-244 N-termi	5.66e-09	
4	159	100.0		R23645	GAD65	.66e-	
ហ	159	100.0	540 1	R59520	1-45 N		
6	159	100.0	544 1	R59524	GAD65 545-585 C-termin	5.66e-09	
7	159	100.0	554 1	R59518	GAD65 1-31 deleted, C4		
œ	159	100.0	584 1	W86017	u	.66e-	
9	159	100.0	584 1	W34519	Human GAD65 protein.	.66e-	
10	159	100.0	585 1	R79105	Human glutamic acid de	5.66e-09	
, 11	159	100.0	585 1	R28756	Human pancreatic islet	.66e-	
12	159	100.0	585 1	W35361	Human 65K-glutamic aci	.66e-	
13	159	100.0	585 1	R29629	Human GAD 65.		
14	159	100.0	585 1	R59516		.66e-	
15	159	100.0	585 1	W12402	65 kD human glutamic a	5.66e-09	
16	159	100.0	585 1	R71641	Human GAD.	.66e-	
17	155	97.5	20 1	R72277	Glutamic acid decarbox	.57e-	
18	148	93.1	341 1	R59523	GAD65 1-244 N-terminal	e-0	
19	148	93:1		R59521	GAD65 1-45 N-terminal-	:	
20	148	93.1	544 1	R59525	545-5	٠	
21	148	93.1	554 1	R59519		.32e-	
22	148	93.1	584 1	W86018	Rat GAD65 protein sequ	. 32e-	
23	148	93.1	584 1	W34520	protein.	.32e-	

Re

45	44	43	42	. 41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	. 25	t,
87	87	91	91	101	103	109	112	112	112	112	121	122	122	126	147	147	148	. 148	148	148	
54.7	54.7	57.2	•	63.5	•	68.6	70.4	70.4	70.4	70.4	76.1	76.7	76.7	79.2	92.5	92.5	93.1	93.1	93.1	93.1	
493	493	506	506	13	594	181	594	594	593	181	23	14	14	20	585	585	605	594	585	585	
Н	سر	۳	μ	Н	ட	<u>ب</u>	بر	۳	μ	ب	H	⊣	Н	ш	щ	ட	Н	Н	H	۳	1
W22306	W20065	W22305	W20064	W35531	R27222	R27218	R27221	W74716	R27220	R27219	R29627	R76653	W18861	W10300	W14915	W14916	R71733	W74717	R29628	R59517	
Human GADII.	Human GADII protein.	Rat GADII.	Rat GADII protein.	Glutamic acid decarbox	Full length islet GAD.	Brain GAD.	Full length brain GAD.	Amino acid sequence of	Brain GAD #2.	Islet GAD.	GAD peptide.	Peptide derived from h	65 kD Glutamic acid de	Mammalian GAD 65 pepti	Modified glutamic acid	Modified glutamic acid	Rat glutamic acid deca	Amino acid sequence of	Rat GAD 65.	Rat GAD65.	יייים טיייטן טיייטן איייים איייי
2.78e-01	2.78e-01	1.10e-01	1.10e-01	1.03e-02	6.38e-03	1.50e-03	7.25e-04	7.25e-04	7.25e-04	7.25e-04	8.00e-05	6.25e-05	6.25e-05	2.32e-05	1.20e-07	1.20e-07	9.32e-08	9.32e-08	9.32e-08	9.32e-08	

ALIGNMENTS

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RESULT 2
ID W18843 standard; peptide; 20
AC W18843;
DT 05-JAN-1998 (first entry)
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Claim 1; Page 12; 15pp; German.

Claim 1; Page 12; 15pp; German.

Chaim 1; Page 1
                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative
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W01794;
15-OCT-1997 (first entry)
Human-652kbcglutamine decarboxylase peptide.
Human; glutamine decarboxylase; GAD: diagnosis; predisposition; tumouf; immunological; disease; autoimmune; diabetes; reagent; determination; T cell; subpopulation; medicament; treatment; prevention; production; antigen; immunogen; tolerogen; isolation; reinjection; inactivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BOEF ) BOEHRINGER MANNHEIM GMBH.
Albert W, Boitard C, Endl J, Jung G, Schendel D;
Stahl P, Van Endert P;
WPI; 97-078452/08.
Glutamine decarboxylase peptide(s) - for diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-1997.
14-JUL-1995; 025784.
14-JUL-1995; DE-025784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
DE19525784-A1.
                                                                                                                                                                                              Score 159; DB 1;
Pred. No. 5.66e-09;
0; Mismatches 0
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TRESULT REPORT OF PROPERTY OF 
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pp 09-JUN-1994; U11705.

R (03-DEC-1992; U5-984935.

R (REGC) UNIV CALIFORNIA.

REGC) UNIV CALIFORNIA.

Regcc) UNIV CALIFORNIA.

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Best Local
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                                                                                                                                                     Matches
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W18842-70 are peptide fragments of the 65 kD human glutamic acid decarboxylase (GAD). The fragments are autoreactive substances used for diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is determined by using a claimed method for diagnosis of cell-mediated diseases or a predisposition to cell-mediated diseases, which is effected by administering an autoreactive substance intradermally and establishing the diagnosis on the basis of the occurrence or lack of a positive reaction at the site of administration. The method is used for diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated diseases such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAD65 1-244 N-terminal-deleted mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R5952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO sapiens.
WO9412529-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stiff man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R59522 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19526561-A1.
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                                             SNMYAMMIARFKMFPEVKEK 21
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Pred. No. 5.66e-09
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No. 5.66e-09;
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Matches 2
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(REGC ) UNIV CALIFORNIA.
(REGC ) UNIV OF CALIFORNIA.
Erlander MG, Kaufman DL, Tobin A.
WPI, 92-150489/18.
N-PSDB; Q24184.
New soluble fragments of glutamic acid decarboxylase protein - used for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome.

Disclosure; Fig. 1; 73pp; Anglish.
The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59518) were determined. New soluble fragments of GAD65 (R59518-5) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for different classes of GAD65 autoantibodies.

Sequence 540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAD65 1-45 N-terminal-deleted mutant. GAD65; glutamate-decarboxylase; diabetes mellitus; stiff man syndrome; autoantibody; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R59520
R59520;
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Glutamic acid dec
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03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                    Baekkeskov S, Kim J,
WPI; 94-200193/24.
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21-SEP-1990; US-586536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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Similarity 100.0%;
20; Conservative
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Pred. No. 5.66e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stiff man
                                                                                                                                                                                                                                                                                            Richter
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Query Match Best Local Similarity

100.0%;

Score Pred.

159; DB 1; No. 5.66e-09

Length

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SNMYAMMIARFKMFPEVKEK SNMYAMMIARFKMFPEVKEK

20

R59524 standard;

protein;

GAD65 545-585 C-terminal deleted mutant. GAD65; glutamate-decarboxylase; diabetes mellitus; stiff man syndrome; autoantibody; mutagenesis.

(first entry)

Matches

20;

Conservative

0;

Mismatches

0

Indels

0

Gaps

201

RESOLDER AND SOLDER AN

SHomo sapiens.

W99412529-A.

W99412529-A.

D3-JUN-1994; U1705.

PF 02-DEC-1993; U1705.

PF 02-DEC-1993; U1705.

PR (REGC) UNIV CALIFORNIA.

P

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S
Query Match
                                      New soluble fragments of glutamic acid decarboxylase protein used for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome.

Disclosure: Fig. 1: 73pp: English.

The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for different classes of GAD65 autoantibodies.
                                                                                                                                                                                                                                                                                                               GAD65 1-31 deleted, C45A mutant.
GAD65; glutamate-decarboxylase; diabetes mellitus; stiff man syndrome; autoantibody; muraronocitoms saries.
                                                                                                                                                                                                09-JUN-1994, U11705.
02-DEC-1993; U11705.
03-DEC-1992; US-984935.
03-DEC JUNIV CALIFORNIA.
(REGC ) UNIV CALIFORNIA.
Baekkeskov S, Kim J, Namchuk M, Baekkeskov S, Kim J, Namchuk M, WPI; 94-200193/24.
                                                                                                                                                                                                                                                                                                                                                                                                        R59518
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                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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100.0%;
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Score
159;
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В
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Best Local (
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.

US5849506-A.

15-DEC-1998.

25-MAY-1995; 450755.

02-DEC-1993; US-161290.

03-DEC-1993; US-984935.

25-MAY-1995; US-450755.

(REGC) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                        Homo sapiens.
US5691448-A.
US5691497.
25-NOV-1997.
02-DEC-1993; US-161290.
02-DEC-1993; US-161290.
03-DEC-1992; US-984935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W34519
W34519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes and stiff man syndrome Examples: Fig 1; 31pp; English.

This represents a human GAD55 protein sequence. The invention provides soluble fragments of GAD65 that are specifically reactive with at least one class of GAD65 autoantibody. The fragments are substantially free of N-terminal amino acids that would otherwise limit solubility. Different fragments contain different epitopes for different classes of GAD65 autoantibodies. These fragments are used in the methods of the invention for detection of GAD65 autoantibodies. These fragments are used for monitoring insulin-dependent diabetes mellitus (IDDM) and stiff man syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 8
W86017
W86017;
                                               Backkeskov S, Kim J, Namchuk M, Richter W, Shi
WPI; 98-017711/02
Soluble fragments of glutamic acid decarboxylas
distinguish between insulin-dependent diabetes
                                                                                                                                                  (RICH/)
                                                                                                                                                                                                                                                                                                                                                                                                                               GAD65; glutamic acid decarboxylase protein; human; soluble fragment; autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis; stiff man syndrome; therapy.
                                                                                                                                                                                                    (BAEK/) BAEKKESKOV (KIMJ/) KIM J. (NAMC/) NAMCHUK M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GAD65
GAD65; gluta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y; WPI; 99-069720/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GAD65
GAD65; auto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 SNMYAMMIARFKMFPEVKEK
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                                                                                                                                               SHI Y.
                                                                                                                                                                            NAMCHUK M.
RICHTER W.
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Similarity 100.0%;
20; Conservative
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antibody; soluble; detection; diagnosis; monitor;
andent diabetes mellitus; stiff man syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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0; Mismatches 0;
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Pred. No. 5.66e-09;
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English
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                                                                              decarboxylase GAD65 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for diagnosis
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Query Match Best Local S Matches 2

h 100.0%; Similarity 100.0%;

Score 159; DB 1; Pred. No. 5.66e-09;

Length 544;

Mismatches

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0

Conservative

or MICA2.

improve

solubility. 544 AA;

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RESULT
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AC R:
AC R:
DT 20
DE H
DE H
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ON H
OPD 20
PD 20
PD 10
PR 11
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Best Local
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Best Local
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W09220811-A.
26.NOV-1992.
14-MAY-1992: U04079.
15-MAY-1991: US-702162.
(UNIW) UNIV WASHINGTON.
(ZYMO) ZYMOGENETICS INC.
FOSTER DC, GRUBIN CE, Hago
WPI; 92-415789/50.
                                                                                                                                                                                                                                  Human
GAD; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human glutamic acid decarboxylase protein GAD65. The invention relates to soluble fragments of a GAD65 protein that are specifically reactive with a GAD65 autoantibody (AAb), where the fragment is at least 99% pure and the AAb binds to a conformational epitope of the fragment. The soluble GAD65 fragments can be used to distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff man syndrome. They can also be used for diabetes mellitus (IDDM) and stiff man syndrome. The fragments can distinguish different temporal and stiff man syndrome. The fragments can distinguish different temporal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide fragments of glutamic acid decarboxylase - for diagnosis and treatment of auto:immune disease, esp. insulin dependent diabetes, also related nucleic acid, vectors, antibodies, hybridoma(s) etc.

Example 1; Fig 3; 100pp; English.

086481 and 086482 encode R71733 and R79105, rat and human glut acid decarboxylase (GAD65) respectively, from which the GAD65 fragments described in R72261-R7298 were derived. These fragment disease to detect autoantibodies against GAD, e.g. to diag and treat GAD-related autoimmune disorders, such as insulin dependent diabetes mellitus or stiff man disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-1994; U09478.
17-SEP-1993; US-123859.
(REGC ) UNIV CALIFORNIA.
Clare-Galzler MJ, Erlander MG,
WPI; 95-131360/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9507992-A
23-MAR-1995
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                    R28756;
R28756;
20-APR-1993 (fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin-dependant diabetes mellitus; stiff man disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat glutamic acid decarboxylase; GAD65; auotimmune disorders;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SNMYAMMIARFKMFPEVKEK
                                                                                                                                                                                                                                  n pancreatic islet cell glutamic acid decarboxylase.
insulin dependent diabetes melting; IDDM; autoantibody detection
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Similarity 100.0%;
20; Conservation
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Similarity 100.0%;
20; Conservative
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decarboxylase (GAD65).
                                                                                                                                                                                                                                                                                      entry)
                            Hagopian
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Pred. No. 5.66e-09;
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No. 5.66e-09;
                                  Karlsen
                               ΑE,
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as insulin
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01-APR-1996; JP-078878.

(CHUS) CHUGAI SEIYAKU F

Kure S, Muto Y, Narisaw

WPI; 97-502847/46.
Homo sapiens.
EP-519469-A.
23-DEC-1992.
                                                                                    R29629;
05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q31783.

Polynucleotide encoding human islet glutamic acid decarboxylase - polynucleotide encoding human islet glutamic acid decarboxylase - used to test for auto-antibodies against itself to diagnose insulin dependent diabetes mellitus pisclosure; Fig 2; 45pp; English.

The sequence is that of human pancreatic islet glutamic acid decarboxylase (GAD) which is used to test biological samples for the presence of autoantibodies to human GAD. It can also be used to remove antibodies against GAD from plasma in order to treat an autoimmune response to GAD, e.g. in insulin-dependent diabetes melting (IDDM), and may also be used to induce immunological tolerance to GAD by giving GAD that specifically binds the GAD receptor on immature T
                                                                                                                                                                                                                                                                                                                                 partial peptide(s) - for diagnosing diseases associated with auto:Immune reaction
Claim 8; Page 14-16; 32pp; Japanese.
A composition has been developed for diagnosing diseases associated with autoimmune reaction caused by 65K-glutamic acid decarboxylase (GAD65) or its partial peptides. The composition reacts with T cells in and/or on the surface of mammalian skin to cause inflammation. The present sequence represents human GAD65. GAD65 and its partial peptides are used to diagnose diseases associated with autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; human; glutamic acid decarboxylase; GAD65; diagnosis; autoimmune reaction; T cell; mammalian skin; autoimmune disease; insulin independent diabetes; inflammation.
                                          Glutamic acid decar
diabetes mellitus;
                                                                                                              T 13
R29629 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition containing 65K-glutamic partial peptide(s) - for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by giving GAD or B cells.
                                                                      Human GAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1998 (first enti
Human 65K-glutamic acid
                                                                                                                                                                                                                                                                                                         simple
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                                        decarboxylase; auto immune
itus; drug screening; antibo
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Narisawa K,
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1. No. 5.66e-09;

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                                           antibody;
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                                                       disease;
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objun-1994.

objun-1993; U11705.

pp 02-DEC-1993; U19-984935.

A (REGC) UNIV CALIFORNIA.

A (REGC) UNIV CALIFORNIA.

New Soluble fragments of glutamic acid decarboxylase protein - used for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome.

T used for the diagnosis and treatment of of insulin dependent diabetes mellitus and stiff man syndrome.

T classes it is 73pp; English.

Disclosure; Fig. 1; 73pp; English.

C The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for GAD65 autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT Glutamic acid decarboxylase isolated polypeptide(s) - useful for daynosis and treatment of auto-immune diseases, e.g. insulin dependent diabetes mellitus, drug screening and antibody prodn. PS Disclosure; Fig 3; 35pp; English.

The DNA encoding glutamic acid decarboxylase (GAD 65) was obtd. by standard recombinant DNA techniques. The protein, or fragments of it, may be used for the detection of autoantibodies to GAD 65. It can also be used for screening drugs such as those that alter GAD 65. Such methods can be used in the diagnosis and therapy of autoimmune diseases such as insulin dependent diabetes mellitus and "stiff man" syndrome. The protein can be used to rblock the continuance of an autoimmune response to GAD 65.

It may also be coupled to therapeutic agents and used immunothera-sec and sec also R29625-8.
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Matches
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Matches 20; Conservative
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18-JUN-1991; US-716909.

(REGC ) UNIV CALIFORNIA.

Clare-Salzier MJ, Erlander MG, WMPI; 92-425701/52.

N-PSDB; Q32760.
 W12402;
08-OCT-1997
65 kD human
                                                   LT 15
W12402
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R59516 standard; protein;
R59516;
R99-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAD65; glutamate-decarboxylase; diabetes mellitus; stiff man syndrome; autoantibody.
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GAD65; glut
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nes 20; Conservative
OCT-1997 (first entry) kD human glutamic acid decarboxylase isoform.
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                                                     standard;
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                                                     Protein;
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Pred. No. 5.66e-09;
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0; Mismatches 0;
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Search completed: Tue Job time : 5 secs.

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1 SNMYAMMIARFKMFPEVKEK

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PT New human glutamic acid decarboxylase peptide(s) - used for process.

PT treatment, diagnosis and determining predisposition to diabetes and process.

PS Disclosure, Fig 1; 28pp; English.

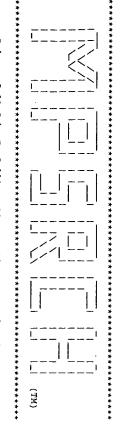
CC This sequence represents the 65 kD isoform of human glutamic acid concerns ylase (GAD65). GAD is an enzyme expressed in the beta cells of the pancreas, and in neurons of the central nervous system. There are two isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of CC GAD65, and analogues of the fragments, are used in the methods of the cinvention. The methods are for detecting or treating diabetes or a cc predisposition to diabetes. The peptides can also be used for native peptides with selective changes of crucial residues can induce curresponsiveness or change the responsiveness of antigen-specific autoreactive T cells. The peptide analogues compete for binding to MHC can do not cause proliferation of the crucial residues can active peptide-specific T cells.

Sequence 585 AA;
                                                Query Match
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Matches 2
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24-JUN-1996; U10790.
23-JUN-1995; US-494624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens. W09700891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuron; central |
T cell; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas; neuron; central nervous system; type I diabetes; autoimmune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KENN-) KENNEDY INST RHEUMATOLOGY.
(NEUR-) NEUROCRINE BIOSCIENCES INC
(SBAR-) ST BARTHOLOMEW'S HOSPITAL (
246 SNMYAMMIARFKMFPEVKEK
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Mar 7 21:16:05 2000; MasPar time 5.48 Seconds 172.132 Million cell updates/sec

Scoring table: Sequence: Description: Perfect Score: PAM 150 Gap 15 >US-08-981-824-2 (1-20) from US08981824.pep 159 1 SNMYAMMIARFKMFPEVKEK 20

Searched: 142080 seqs, 47172406 residues

Statistics: Databas Post-processing: _Mean_30-041; Variance 49.478; scale 0.607 pir62 1:pir1 2:pir2 3:pir3 4:pir4 Minthum Match 0% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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hypothetical protein probable heme A farne	e-related pro in kinase rck	conserved hypothetica hypothetical protein	-	lutamate decarboxyl	lutamate lutamate	lutamate decarboxy	lutamate	glutamate decarboxyla glutamate decarboxyla	glutamate decarboxyla 65 kda glutamate deca	glutamate decarboxyla	Description
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S62452 B70333	T15194	S37431	в36938	S32607	A40831	S62117	S33364	A39360	JC2437	JC4345	S78662	MRBY	S36389	B69160	T03301	S49942	F69427	H70254	1.1	T04432
probable protein kina hypothetical protein	hypothetical protein	ankyrin 2, neuronal l	acriflavin resistance	trifunctional enzyme	gag-akt polyprotein -	protein kinase B (EC	serine/threonine-spec	protein kinase (EC 2.	RAC protein kinase al		mRNA maturase SCBI2 -	mRNA maturase bI3 - y	protein kinase B (EC	mevalonate kinase - M	rab3 effector protein	hypothetical protein	ਾਹੇ	hypothetical protein	hypothetical protein	protein kinase homolo
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ALIGNMENTS

#authors Mauch, L. #journal Eur. J. B #title Character pancrea autoimm diabete #cross-references MUID: #accession S30058 ##molecule_type mRNA ##residues 6-58	#title Cloning a glutami #cross-references MUID: #accession A41292 ##molecule_type mRNA #residues references 1-58 ##xperimental_sources \$30058	##molecule_type mRNA ##residues 1-58 ##eross-references G ##experimental_sourc ##note A41292 REFERENCE Karlsen, Distech Grant, ##fournal Browner	#authors #journal #title #cross-referent #accession	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel, B.; Northemann, M. #journal Eur. J. Blochem. (1993) 212:597-603 #title Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients. #cross-references MUID:93185681 #accession \$30058 ##molecule_type mRNA ##residues 6-585 ##label MAU	nd primary structure of a cid decarboxylase from 92020848 s ##label KAR B:M74826; NID:g182931; P. B:M74826; NID:g182931; P.	##molecule_type mRNA ##presidues 1-585 ##label BU1 ##cross-references GB:M01882; NID:g182933; PIDN:AAA62367.1; PID:g182934 ##cross-references GB:M01829; NID:g182933; PIDN:AAA62367.1; PID:g182934 ##rote	Hauthors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J. Journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119 Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene. Cross-references MUID:92196068 accession A41935	#type complete glutamate decarboxylase (BC 4.1.1.15) 2 - human glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Homo sapiens #common_name man 13-May-1992 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999 A41935; A41292; S30058; B54778 A41935

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CLASSIFICATION
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Best Local Similarity
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Best Local
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#title
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#title
                                                                                                                                                                                            393-396
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                                                                                                                                                                                                                                                                                                                                                                                                            #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:95137399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
                                                                                                                                                                                                                                                                                                          ##experimental_source brain
                                                                                                                                                                                                                                                                                                                              ##cross-references DDBJ:D31848; NID:g790964; PIDN:BAA06635.1; PID:d1007207; PID:g790965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 SNMYAMMIARFKMFPEVKEK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references GDB:128595; OMIM:138275

p_position 10p11.23-10p11.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:X69936
                                      246 SNMYAMLIARFKMFPEVKEK 265
                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
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سر
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SNMYAMMIARFKMFPEVKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acit has several isoforms, each encoded by a separate gene. GAE also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.
                                                                                                                                                                                                                                                  This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.

FION #superfamily human glutamate decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%;
Similarity 100.0%;
20; Conservative
                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics (1994) 21:222-228
The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M. Gene (1995) 152:257-260
Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig
#formal_name Sus scrofa domestica #common_name domestic pig
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #length
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                                                                                                                                                                                                                                carbon-carbon lyase; carboxy-lyase
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                                                                                                                                                      #length
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                    1-585 ##label SUZ
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                                                                                                                                                                                            #domain
                                                                                                                                                                          #label
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| 585 #molecular-
                                                                                            95.6%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #type complete
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                                                                                                                                                    #molecular-weight 65388
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Pred. No. 4.75e-18;
                                                                          Score 152; DB 2;
Pred. No. 1.55e-16;
1; Mismatches 0
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                                                                                                            Length 585
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                               CLASSIFICATION
                                                                                               COMMENT
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                              **PRENCE A60888

**authors Chang, Y.C.; Gottlieb, D.I.

**journal J. Neurosci. (1988) 8:2123-2130

**title Characterization of the proteins purified with monoclonal

**antibodies to glutamic acid decarboxylase.

**cross-references_MUID:88258610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harr
#journal Endocrinology (1993) 133:2962-2972
Localization and quantitation of expression of
decarboxylase genes in pancreatic beta-cells
peripheral tissues of mouse and rat.
#cross-references MUID:94062679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.; Tobin, A.J.

#journal Neuron (1991) 7:91-100

#title Two genes encode distinct

#cross-references MUID:91299343

#accession JH0423
                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                           ##molecule_type protein

'V', 191-194,'X',196-203,'XX',206-219;'X',225-234,'X',

##residues

'V', 191-194,'X',249-266,'X',524-537,539-543,'V',547-549,

236-247,'X',249-266,'X',524-537,539-543,'V',547-549,

'X',551-53,'X',555-558 ##label CHA

'X',551-53,'X',555-558 ##label CHA

NT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-205 ##label RES
##cross-references GB:S67454; NID:g456852
FFICATION #superfamily human glutamate do
#length 205 #checksum 3167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##experimental_source brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
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it has several isoforms, each encoded by a separate gene.
N #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JH0423 #type complete
glutamate decarboxylase (EC 4.1.1.15) 2 - rat
glutamate decarboxylase GAD65; L-glutamate 1-c
#formal_name Rattus norvegicus #common_name N
#formal_same Rattus norvegicus #common_same N
31-Mar-1992 #sequence_revision 23-Mar-1995 #te
                                                                                                                                                                                                                                          A60888
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JH0423; A60888
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65 kda glutamate decarboxylase, brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erlander, M.G.;
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27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                              the authors translated the His, TCA for residue 198 428 as Trp
                                                                                                                                                                                                             preliminary
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2;
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Pred. No. 1.11e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-glutamate 1-carboxy-lyase 
#common_name Norway rat 
23-Mar-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                          as Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                             codon GAT for residue 86 as
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    phosphoprotein; pyridoxal
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Best Local S
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Matches
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#journal Biochim. Biophys. Acta (1993) 1216:157-160
#title Cloning and sequence analysis of a murine cDNA
glutamate decarboxylase (GAD65).
#cross-references MUID:94032481
#accession S38533
##status
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#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal J. Neurosci. (1987) 7:2768-2772
#title Glutamic acid decarboxylase cDNA: nucleotide
encoding an enzymatically active fusion pro
#cross-references MUID:87310623
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                                                                                                                                                                                                                                                                                             #submission
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##cross-references GB:L16980; NID:g413867; PIDN:AAA93049.1; PID:g413868
NT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
IFICATION #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                            ##residues 1-594 ##label KOB 1-59163858; PIDN:AAA51430.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    glutamate decarboxylase (EC 4.1.1.15) 1 - cat glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase #formal_name Felis silvestris catus #common_name domestic c 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999
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glutamate decarboxylase GAD5; L-glutamate 1-carboxy-lyase
#formal_name Mus musculus #common_name house mouse
20-May-1994 #sequence_revision 23-Mar-1995 #text_change
                                                                                                                                                                    A4567
                                                                                                                                                                                                                                                                                                submitted to GenBank, A46758
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1 585 #molecular-
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Pred. No. 1.11e-15;
""smatches 0;
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##note this sequence has been revised in reference A46758

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
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ENTRY
TITLE
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CLASSIFICATION
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Matches
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Best Local Similarity 70.0%;
Matches 14; Conservative
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                                                                              #journal
                                                                                              #authors
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IFICATION #superfamily human glutamate d
#length 206 #checksum 3323
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##residues 1-558,'RGTRPTFSGWSSRTQLLHSPILTSSSRR' ##label KO2
             ##molecule_type mRNA
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Similarity 70.0%;
14; Conservative
                                                                                                                                                             glutamate decarboxylase (EC 4.1.1.15) 62K iso glutamic acid decarboxylase formal_name Mus musculus #common_name house 19-Mar-1997 #sequence_revision 25-Apr-1997 #t
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#status predicted
#length 594 #molecular-weight 66824 #non-neight
                                         Katarova, Z.; Szabo, G.; Mugnaini, E.;
Eur. J. Neurosci. (1990) 2:190-202
Molecular identification of the 62 kd i
decarboxylase from the mouse.
                                                                                                               S61534; S61533
S61534
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glutamate decarboxylase, 67k, brain - mouse (fragment)
#formal_name Mus sp. #common_name mouse
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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1-585 ##label
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Pred. No. 4.89e-09;
3; Mismatches 3
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Pred. No. 3.05e-08;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                               4.1.1.15) 62K isoform -
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REFERENCE S61533
              COMMENT
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Best Local
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#title
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#accession A41367
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##molecule_type mRNA
1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',
##residues 1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',
348-351,'LE',354-379,'R',381-593 ##label JUL
348-351,'LE',354-379,'R',381-593 ##label JUL
##cross-references GB:X57572; NID:g56185; PIDN:CAA40800.1; PID:g56186
##cross-references GB:X57572; NID:g56185; PIDN:CAA40800.1; PID:g56186
                                                                                                                                                                                                                                                                    ##residues 1-593 ##label WYB
##cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184
##note the authors translated the codon TGT
                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
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PID: g886687
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##residues 1-554,'YQPQGDKANFFRMVISNPAASQSDIDFLTEEIERLGQDL' ##label
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Similarity 70.0%;
                                                                                                                    JH0195
                                                                                                                                                                                          Julien, J.F.; Samama, P.; Mallet, J. Neurochem. (1990) 54:703-705
                                                                                                                                                                                                                                                                                                                                                                                                                                       Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.
Brain Res. Mol. Brain Res. (1990) 8:193-198
Characterization of a cDNA coding for rat glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning, characterization, and autoimmune recognition of islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamate decarboxylase (EC 4.1.1.15) 1 - rat
glutamate decarboxylase GAB67; L-glutamate 1-carboxy-lyase
#formal_name Rattus norvegious #common_name Norway rat
12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the differences at the carboxyl end are due
frameshift error
#superfamily human glutamate decarboxylase
carbon carbon lyase; carboxy-lyase
#length 585 #molecular-weight 65381 #checksum
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                                                                                                                                                                             Rat brain glutamic acid decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                    A43756
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                                                                                                                                                                                                                                      JH0195
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#title
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#cross-references MUID:93080286
#accession $48135
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                                                                                                                                                                                                 #submission
                                                                                                                                                                                                                    authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##COSS references EMBL:222750
IFICATION #superfamily human glutamate decarboxylase
RDS carbon-carbon lyase; carboxy-lyase
RY #length 593 #molecular-weight 66952 #checksum
                                                                                                             ##status preliminary
##molecule_type mRNA
##residues 1-593 ##label JOH
##cross-references_EMBL:222750
                                                                                                                                                                                                                                                                                                                                                                                                                        254 SNMYSIMAARYKYFPEVKTK 273
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Similarity 70.08;
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                                                                                                                                                                                    submitted
S51776
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S51775
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glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo sapiens #common_name man
14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
07-May-1999
                                #superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase #length 593 #molecular-weight 56946 #che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.; Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D. Ann. Hum. Genet. (1992) 56:255-265

Nucleotide sequence and Chromosomal assignment of a cDNA encoding the large isoform of human glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                                                                                                                glutamate decarboxylase (EC 4.1.1.15) - human #formal_name Homo sapiens #common_name man 15-Jul-1995 #sequence_revision 21-Jul-1995 #tm
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                                                                                this is an unpublished revision reference S48135
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70.4%; Score 112;
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Pred. No. 3.06e-08;
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Pred. No. 3.06e-08;
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#journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Yamashita, K.; Cram, D.S.; Harrison, L.C.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title Molecular cloning of full-length glutamic acid decarboxylase
#tross-references MVID:93282844
#cross-references MVID:93282844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Kawasaki, E.; Moriuchi, R.; Watanabe, M.; Saitoh, K.
Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen,
Akazawa, S.; Miyamoto, T.; Nagataki, S.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
#title Cloning and expression of large isoform of glutamic decarboxylase from human pancreatic islet.
#cross-references MUID:93282845
                                                                                                                                                                                                                         #accession
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       #cross-references MUID:91248209
                                                                                                                                                                                                                                             #cross-references MUID:92065769
                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-67,'K',69-435,'L',437-511,'S',513-594 ##label YAM ##cross-references GB:S61897; NID:g385450; PIDN:AAB26937.1; PID:g385451 ##experimental_source pancreatic islet
                                                                                                                                                   ##experimental_source brain
                                                                                                                                                                                              ##molecule_type mRNA
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                                                                                                                                                                            ##residues
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Lancet (1991) 338:1468-1469
Cloning of large isoform of human b
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                              Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, I
Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
Cloning and partial nucleotide sequence of human glu
acid decarboxylase cDNA from brain and pancreatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-Jun-1999
B41935; JH080
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                                                                                                                               PQ0157
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156-301,'C',303-476,'G',478-491,'G',493-594 ##label
                                                                                                                                                                          62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 ##label KEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence extracted from NCBI backbone (NCBIP:88006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119 uman glutamate decarboxylases, 65-kDa GAD and
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Mismatches 3;
                                                                                                                                                                                                                                                                                               of human brain
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                           and pancreatic islet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saitoh, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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#cross-references MUID:92020930

#accession B41367
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p_position 2q31-2q31
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#residues 527-594 ##label PER
##cross-references GB:M55574; NID:g
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##residues 218-.
                                                                                                                                                                          1 SNMYAMMIARFKMFPEVKEK 20
                                                                                                                                                                                                               SNMYSIMAARYKYFPEVKTK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                             70.4%;
Similarity 70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.; Skog, S.; Hoekfelt, T.; Ritzen, E.M.
MOl. Cell. Biol. (199) 10:4701-4711

Expression of the neurotransmitter-synthesizing e
glutamic acid decarboxylase in male germ cells.
glutamate decarboxylase (EC 4.1.1.15) 67K chain - pig
#formal_name Sus scrofa domestica #common_name domestic
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily human glutamate decarboxylase
alternative splicing; carbon-carbon lyase;
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The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and
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Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
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1594 #molecular-weight 66924
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                                                                           #type complete
                                                                                                                                                                                                                                                                                             Score 112; DB 1;
Pred. No. 3.06e-08;
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Best Local Similarity 70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).
#cross-references MUID:95137399
 #journal
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                    #authors
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This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.

IFICATION #superfamily human glutamate decarboxylase
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##residues
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FICATION #superfamily human glutamate decarboxylase
DS carbon-carbon lyase; carboxy-lyase
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PID:d1007208; PID:g790967
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 Reymond, Biochim.
                                                                                                                                         sulfoalanine decarboxylase (EC 4.1.1.29) cysteine sulfinate decarboxylase; cysteine
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glutamate decarboxylasse (EC 4.1.1.15) - human
fformal_name Homo sapiens #common_name man
15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
                                    S71489
                                                      S71489; S78208; S55689;
                                                                                     #formal_name Rattus norvegicus
09-Dec-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                            #length 594
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70.0%;
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I.; Sergeant, A.; Tappaz, M.
Biophys. Acta (1996) 1307:152-156
                                                                                                                                                                             #type complete
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Pred. No. 3.06e-08;
3; Mismatches 3
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Pred. No. 3.06e-08;
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                                                                                     #common_name Norway rat
09-Dec-1997 #text_change
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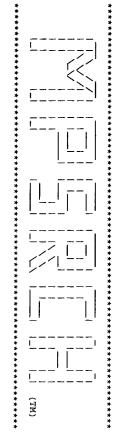
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##molecule_type protein
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#note the author's name has been corrected in reference S60723
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##molecule_type protein
##residues 220-230 ##label KA2
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                                                                                                                 155 SNMYAINLARFORYPDCKOR 174
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PID:g847653
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                                                                            SNMYAMMIARFKMFPEVKEK
                                                                                                                                                     similarity 50.0%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaisakia, P.J.; Jerkins, A.A.; Goodspeed, D.C.; Steele, R.D Biochim. Biophys. Acta (1995) 1262:79-82 Cloning and characterization of rat cysteine sulfinic acid
                                                                                                                                                                                                                                                                                                                           this a correction of the author's name from reference S55689 #superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                                                    S60723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S55690
                                                                                                                                                                                                                                                                                                                                                                                        annotation; erratum
                                                                                                                                                                                                                                                                                                                                                                                                            Kaisaki, P.J.; Jerkins, A.A.; Goodspeed, D.C.; Biochim. Biophys. Acta (1995) 1263:179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S55689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S55689
                                                                                                                                                                                                                                  #length 493 #molecular-weight 55248
                                                                                                                                                                                                                                                                                                               phosphate
                                                                                                                                                                                                                                                    #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9-22;106-124;467-484 ##label REM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-493 ##label REY
                    7 21:16:14 2000
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                                                                                                                                                     Score 91;
Pred. No.
6; Misma
                                                                                                                                                         Mismatches
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3.18e-04;
                                                                                                                                                                                            Length 493
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. MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:15:41 2000; MasPar time 3.44 Seconds 173.487 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-981-824-2 (1-20) from US08981824.pep 159

1 SNMYAMMIARFKMFPEVKEK 20

Scoring table: PAM 150 Gap 15

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 30.741; Variance 44.172; scale 0.696

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22210987543321 222109875543321 232109875543321	Result
159 1488 11488 1112 1112 1112 1112 1112 111	Score
100.0 93.6 93.1 70.4 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 44.5 3.0 45.5 45.5 45.5 45.5 45.5 45.5 45.5 45	Query Match
1 9 5 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5	Length
	BB BB
DCE2_HUMAN DCE2_PIG DCE2_MOUSE DCE2_RAT DCE1_FELCA DCE1_RAT DCE1_PIG DCE1_PIG DCE2_DROME MAK_MOUSE YEAST KIME_METTH MB12_YEAST KRAC_BUMAN KRAC_MOUSE KRAC_RAT KRAC_ROUSE KRAC_RAT KRAC_ROUSE	ID
GLUTAMATE DECARBOXYLAS SERINE/THREONINE-PROTEIN HYPOTHETICAL 65.3 KD P MEVALONATE KINASE (EC CYTOCHOME B MRNA MATU RAC-ALPHA SERINE/THREO	Description
5.32e-21 2.65e-18 2.65e-18 2.65e-11 7.41e-10 7.41e-10 7.41e-10 7.41e-10 7.41e-10 1.36e-01 1.36e-01 1.36e-01 1.36e-01 3.50e+00	Pred. No.

RΤ

sera from insulin-dependent diabetes mellitus patients.";

4 4 5	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24
60 0	60	60	60	60	61	61	61	13	51	61	61	61	61	62	62	6 3	53	63	6 ω	64
37.7 37.7	37.7	37.7		37.7					38.4	38.4								39.6		
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QOX1_ACEAC PHLD_BOVIN	VNS1_EHDV2	PRTP_MOUSE	ENO_SCHMA	YQHG_ECOLI	N120_YEAST	GLYA_TREPA	C6B6_HELAM	C6B2_HELAM	KRCB_RAT	KRCB_HUMAN	Y114_NPVAC	xGCU_ECOLI	PCP_LACIC	ACRF_ECOLI	YRO1_CAMJE	HGT1_KLULA	KAA8_SCHPO	P53_MESAU	P53_CRIGR	ANKB_HUMAN
UBIQUINOL OXIDASE POLY PHOSPHATIDYLINOSITOL-G	NONSTRUCTURAL PROTEIN	LYSOSOMAL PROTECTIVE P	ENOLASE (EC 4.2.1.11)	HYPOTHETICAL 35.1 KD P	NUCLEOPORIN NUP120 (NU	SERINE HYDROXYMETHYLTR	6B6 (CYTOCHROME P450 6B2 (E	RAC-BETA SERINE/THREON	RAC-BETA SERINE/THREON	HYPOTHETICAL 49.3 KD P	HYPOTHETICAL 23.3 KD P	PYRROLIDONE-CARBOXYLAT	ACRIFLAVIN RESISTANCE	HYPOTHETICAL 107.7 KD	HIGH-AFFINITY GLUCOSE	PROBABLE SERINE/THREON	CELLULAR TUMOR ANTIGEN	CELLULAR TUMOR ANTIGEN	ANKYRIN, BRAIN VARIANT
1.60e+01 1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	7.55e+00	7.55e+00	5.15e+00		5.15e+00	5.15e+00	3.50e+00

ALIGNMENTS

RES	1
AC L	DCEZ_HUMAN STANDARD; PRT; 585 AA.
DT.	(Rel. 33,
DT	01-FEB-1996 (Rel. 33, Last sequence update)
ΡŢ	(Rel. 33, Last annotation update)
DE	CARBOXYLASE, 6
DE	
GN	GAD2 OR GAD65.
SO	sapiens (Human)
გ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
8	nidae; Homo.
RN	
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 92196068.
RA	BU DF., ERLANDER M.G., HITZ B.C., TILLAKARATNE N.J., KAUFMAN D.L.,
RA	
RT	"Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
RT	
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
R	
77.	SECOENCE FROM N.A.
R R	MEDLINE; 943/5018.
RT	ි බ
RT	(GAD67 and GAD65) sugges
꼽	ive from a common ancestral GAD.";
Ž	GENOMICS 21:222-228(1994).
RN	[3]
RP	
RC	TISSUE=PANCREATIC ISLETS;
RX	MEDLINE; 92020848.
RΑ	PIAN W.A., GRUBIN C.E., DUBE S.,
RA	ARMEIER H., MATHEWES S., GRANT F.J., FOSTER D.,
RA	
RΤ	"Cloning and primary structure of a human islet isoform of glutamic
RT	decarboxylase from chromosome 10.";
RL	Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).
RN	
RΡ	SEQUENCE OF 6-585 FROM N.A.
RC	ANCREAS;
RX	MEDLINE; 93185681.
RA	MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEDVOGEL B.,
RA	NW.;
RT	"Characterization of a linear epitope within the human pancreatic
RI	decarboxylase and

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Best Local S
Matches
the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@ish-sih h
                                                                                                                                                                                                                                                                                                                       SuS
                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_dec; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxyla
Pyridoxal_phosphate; Multigene family.
BINDING 396 396 PYRIDOXAL_PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M74826; AAA58491.1; -.
EMBL; X69936; CAA49554.1; ALT_INIT.
EMBL; M70435; AAA52513.1; -.
PIR; A41292; A41292.
PIR; PQ0158; PQ0158.
MIM; 138275; -.
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                                                                                                                                                                                      Gene
                                                                                                                                                                                                  "Sequences of two porcine 67-kDa GAD).";
                                                                                                                                                                                                                         SUZUKI R., ASAMI N.,
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                 P48321;
01-FEB-1996
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                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 SNMYAMMIARFKMFPEVKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e by non-profit institutions as long as its content is in no way diffied and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _
                                                                                                                 FUNCTION: CATALYZES THE PRODUCTION OF CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AN COFACTOR: PYRIDOXAL PHOSPHATE: SUBUNIT: HOMODIMER (BY SIMILARITY). SIMILARITY: BELONGS TO GROUP II DECARE
                                                                                                        TYRDC).
                                                                                                                                                                                                                                                                                                                   2 OR GAD65.
scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                             KD GLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-GLUTAMATE COFACTOR: PYRIDOXAL PHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biochem. 212:597-603(1993). FUNCTION: CATALYZES THE PRODUCTION OF GABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DECARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                      152:257-260(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNMYAMMIARFKMFPEVKEK
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Similarity 100.0%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65411 MW;
                                                                                                                                                                                                                           AMANN E.,
                                                                                                                                                                                                                                                                                                                                              DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                              glutamic acid
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Pred.
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                                                                                                                                                                                                                            WAGATSUMA M.;
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                                                                                                                  II DECARBOXYLASES
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                                                                                                                                                                                                                                                                                                                                                                                                                            585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ); DB 1;
. 5.32e-21
                                                                                                                                                           4-AMINOBUTANOATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Decarboxylase;
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                                  There are no restrictions ong as its content is in
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                                                                                                                                                                                                             decarboxylases (65-
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                                                                                                                                                                       GABA
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                                                                                                                     GAD,
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Best Local
                                                                                                                                                                                           decarboxylase genes in pancreatic beta-cel tissues of mouse and rat."; Endocrinology 133:2962-2972(1993).
-!- FUNCTION: CATALYZES THE PRODUCTION OF -!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AM -!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCE2_MOUSE STANDARD; PRT; 585 AA.
P48320; O35519;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00282; pyridoxal_deC; 1.

meurotransmitter biosynthesis; Lyase; Decarbox; Pyridoxal phosphate; Multigene family.

BINDING 396 97RIDOXAL PHOSPHA SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;
                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              ASADA H., KAWAMURA Y., MARUYAMA K., KUME H., DING R.G., JI F.Y., KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.; "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase (GAD5) maintain normal levels of GAD57 and GABA in their brains are susceptible to seizures.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAD2
                                                                           esu
                                                                                                    This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and sequence decarboxylase (GAD65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6; TI
MEDLINE; 94032481.
LEE D.S., TIAN J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D31848; BAA06635.1; PROSITE; PS00392; DDC_GAD_
                                                                                                                                                                  -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE,
                                                                                                                                                                                                                                                                        "Localization and quantitation of expression of +--- decarboxylase genes in ---
                                                                                                                                                                                                                                                                                                                         MEDLINE; 94062679
                                                                                                                                                                                                                                                                                                                                       TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; T
MEDLINE; 97115675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                        the European
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 175-379 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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                                                                        pean Bioinformatics Institute. There are no rest
non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                 Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIAN J., PHAN T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , N.A.
/6; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acta 1216:157-160(1993).
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sis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 152; DB 1;
Pred. No. 2.80e-19;
                                                                                                                                                                                                                                                                                                                                                                                 229:891-895(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                         expression of two glutamate beta-cells and other periph
                                                                                                                    It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.L.;
                                                                                                                                                                                                               4 - AMINOBUTANOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Decarboxylase
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                                                                                                                                                                                                                             GABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1.1.15) (GAD-65)
                                                                                                                                                                   AND TO PLP-TYPE HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                         and
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                                                                                                       the
                                                                                      restrictions
                                                                                                                                                                                                               +
                                                                                                                                                                                                                                                                         peripheral
                                                                                                      EMBL outstation
                                                                                                                                                                                                               CO(2)
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EMBL; L16980; AAA93049.1;

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RESULT PROCESS OF THE PROCESS OF THE
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( EMBL; M72422; AAA63488.1; -.

R PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.

R PFAM; PF00282; pyridoxal_dec; 1. Lyase; Decarboxylase; (W Neurotransmitter biosynthesis; Lyase; Decarboxylase; weurotransmitter biosynthesis; Dyridoxal phosphate; Multigene family.

Pyridoxal phosphate; Multigene family.

Pyridoxal phosphate; Multigene family.

PYRIDOXAL PHOSPHATE (PC 75.07) MW; E35D601A CRC32;
                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCE2_RAT
Q05683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
(65 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYZIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTE
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two genes encode dis
Neuron 7:91-100(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAD2 OR GAD65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: $67454; CAB32806.1; MGD; MGI:95634; GAD2.
PROSITE: PS00392; DDC_GAD_HDC_YDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurotransmitter
Pyridoxal phosph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00282; pyridoxal_deC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOBIN A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERLANDER M.G., TILLAKARATNE N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-HIPPOCAMPUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                               246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 SNMYAMLIARYKMFPEVKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DECARBOXYLASE.
                              SNMYAMLIARYKMFPEVKEK
  SNMYAMMIARFKMFPEVKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D42051; BAA22893.1;
S67454; CAB32806.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ansmitter biosynthesis; Lyase; Dal phosphate; Multigene family.

396 396 PYRIDOXAL F

259 259 F -> S (IN 1 325 325 K -> E (IN 1 499 499 P -> S (IN 1 585 AA; 65224 MW.
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
18; Conse
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                                                                                             93.1%;
larity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        distinct glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
                                               265
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  20
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Pred. No. 2.:
2; Mismatc
                                                                                               Pred.
2; 1
                                                                                                                      Score 148; DB 1;
Pred. No. 2.65e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRIDOXAL PHOSPHATE (POTENTIAL).

I -> S (IN REF. 2).

I -> S (IN REF. 2).

K -> E (IN REF. 2).

P -> S (IN REF. 2).

9BE5C088 CRC32;
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                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELDBLUM S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      decarboxylases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N OF GABA.
4-AMINOBUTANOATE +
                                                                                                                                                                                                                                                                   Decarboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Decarboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le
?.65e-18;
ches 0;
                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATEL
                                                                                                                                          Length 585
                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO PLP-TYPE HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                               Gaps
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Best Local S
Matches 1
                                                                                                                                                                                                                 OCE1_MOUSE STANDARD; PRT; 593 AA P48318; P48318; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) O1-FEB-1996 (Rel. 33, Last annotation update GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-stb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCE1_FELCA STANDARD; PRT; 594 AA.
P14748;
01-APR-1990 (Rel. 14, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15)
(67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00282; pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family.

BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (67 KD GLUTAMIC ACID DECARBOXYLASE)
GAD1 OR GAD67.
                                                 SEQUENCE FROM TISSUE-BRAIN;
                                                                                                                                                   Eukaryota;
                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                       GAD1 OR GAD67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A45671; A45671.
PIR; A46758; A46758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-1- CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANC
-1- COFACTOR: PYRIDOXAL PHOSPHATE.
-1- SUBUNIT: HOMODIMER.
-1- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzymatically active fusion protein."; J. Neurosci. 7:2768-2772(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-OCCIPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata;
                               KATAROVA
                                                                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M18629; AAA51430.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOBAYASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 87310623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;
Glutamic acid decarboxylase cDNA: nucleotide
     (ATAROVA Z., SZABO G., MU(
Molecular identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYRDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNMYAMMIARFKMFPEVKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNMYSIMAARYKFFPEVKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                            Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 AA;
                                                                                                                              (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                           N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%;
                                                                                                                         Chordata; Craniata; Ve. Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fissipedia;
  MUGNAINI E.,
ion of the 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 116; DB 1;
Pred. No. 9.26e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
lia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3EC20778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
  GREENSPAN R.;
kd form of gl
                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 - AMINOBUTANOATE
form of glutamic
                                                                                                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32;
                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                      4.1.1.15) (GAD-67)
                                                                                                                              Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GAD-67)
     acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ACC CONTRACT RANGE OF THE RESERVE OF
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Best Local S
Matches 1
"Rat brain glutamic cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                            P18088;
01-NOV-1990 (
01-NOV-1990 (
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
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EMBL; S67
MGD; MGI:
PROSITE;
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
(67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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-!- FUNCTION: CATALYZES THE PRODUCTION OF
-!- CATALYZIC ACTIVITY: L-GLUTAMATE = 4-AN
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decarboxylase genes in pancreatic beta-cells and oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                                                                                       GAD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCE1_RAT
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                                                                                                                                   Brain
                                                                                                                                                      decarboxylase.
                                                                                                                                                                                         WYBORSKI R.J., BOND
                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           Eutheria;
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SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC
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                                  ., SAMAMA
glutamic
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larity 70.0%;
Conservative
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360
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                                     decarboxylase
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                                                                                                                                                                      GOTTLIEB
NA coding
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Pred. No. 7.41e-10;
                                                                                                                                   8:193-198(1990
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E -> K (IN REF. 2).
S -> T (IN REF. 1).
D -> S (IN REF. 1).
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for rat glutamic
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                                  sequence
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ae; Murinae;
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Rattus.
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                                     a cloned
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PIR; A43756; A43756;

POSITE; PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_deC; 1.

Neurotransmitter biosynthesis; Lyase; De
Pyridoxal phosphate; Multigene family.

BINDING 404 404 404

CONFLICT 103 103 L-> V (IN
CONFLICT 284 284 E.-> S (IN
                                                                                                                                                                                                                                            DCE1_HUMAN STANDARD; PRT; 594 AA. 999259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 92925959; 929259; 929259; 929259; 929259; 929259; 929259; 929259; 92
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[3]
SEQUENCE FROM
MEDLINE; 92020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       GAD1
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-:- CATALYZIC ACTIVITY: L-GLUTAMATE = 4-AMINOBU-
-:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- SUBUNIT: HOMODIMER.
-:- SIMILARITY: BELONGS TO GROUP II DECARBOXYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, characterization, and glutamic acid decarboxylase in Proc. Natl. Acad. Sci. U.S.A. 8
                                         MEDLINE; 92196068.
BU D.-F., ERLANDER
WAGNER-MCPHERSON C.
                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M34445; AAC42037.1; -.
EMBL; X57572; CAA40800.1; -.
EMBL; X57573; CAA40801.1; -.
EMBL; M76177; AAA41184.1; -.
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                                                                                                             SEQUENCE FROM N.A
TISSUE=BRAIN;
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ERLANDER M.G., HITZ B.C., TER-MCPHERSON C.B., EVANS G.A., Thuman glutamate decarboxylases, encoded by a single gene.";
                                                                                                                                                                                                                                       OR GAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
14; Conser
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AG -> EA (IN REF. 2).
T -> I (IN REF. 2).
FD -> LE (IN REF. 2).
L -> R (IN REF. 2).
W; 5A0B67CO CRC32;
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                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e 112; DB 1; Len
. No. 7.41e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              II DECARBOXYLASES
                          , TILLAKARATNE N.J.,
TOBIN A.J.;
s, 65-kDa GAD and 67-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Phis sward the Swiss Institute the European Bioinformatics Institute. The the European Bioinformatics Institutions as long modified and this statement is not removed modified and this statement (Secondary of the statement (Secondary) increased (Secondary).
                                                                                                                                                                                                                                                                                                           CRAM D.S., BARNETT L.U., "Cloning and partial nuc decarboxylase cDNA from Biochem. Biophys. Res. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE;
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KELLY C.I
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TISSUE-PANCREATIC
MEDLINE; 93282845.
                                                                                                                                                                                   decarboxylase in male germ cells.";
Mol. Cell. Biol. 10:4701-4711(1990).
-i- FUNCTION: CATALYZES THE PRODUCTION
-i- CATALYTIC ACTIVITY: L-GLUTAMATE = 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAWASAKI E., MORTUCHI R., WATANABE M., SAITOH K., BRUNICARDI WATT P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.; "Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELLY C.D., EDWARDS Y., JOHNSTONE A.P. MUSSEY S.S., POVEY S., CARTER N.D.; "Nucleotide sequence and chromosomal the large isoform of human glutamate Ann. Hum. Genet. 56:255-265(1992).
                                                                                                                                                                                                                               PERSSON H., PELTO-HUIKKO M., METSIS M., SOEDER O SKOG S., HOEKFELT T., RITZEN E.M.; "Expression of the neurotransmitter-synthesizing
                                                                                                                                                                                                                                                                               SEQUENCE OF
TISSUE=TESTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAMASHITA K., CRAM D.S., HARRISON "MOLECULAR Cloning of full-length human pancreas and islets.";
Biochem. Biophys. Res. Commun. 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The exon-intron organization of the two human glutamate decarboxylases (they derive from a common ancestral cgenomics 21:222-228(1994).
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L16888;
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glutamic acid decarboxylase
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01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC
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BINDING
This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf the European Bioinformatics Institute. use by non-profit institutions as 1
                                                                                                                                                                                                               "Sequences of two porc 67-kDa GAD)."; Gene 152:257-260(1995)
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Neurotransmitter biosynthesis;
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CATALYTIC ACTIVITY: L-GLUTANATE - 4-AMINOBUTANO
CATALYTIC ACTIVITY: L-GLUTANATE - GAMINOBUTANO
COFACTOR: PYRIDOXAL PHOSPHATE.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBUNIT: BELONGS TO GROUP II DECARBOXYLASES
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                                        EMBL
                                        a collaboration - MBL outstation
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Best Local
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                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM: PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase;
Neurotransmitter biosynthesis; Lyase;
Pyridoxal phosphate; Multigene family.
                                                                                                Pyridoxal phosphate.
BINDING 322 3
SEQUENCE 510 AA;
                                                                                                                                               FLYBASE; FBgn0004516; Gad1.
PROSITE; PS00392; DDC_GAD_HDC_YDC;
PFAM; PF00282; PYridoxal_deC; 1.
                                                                                                                                                                                      PIR; A30999; A30999.
PIR; JH0192; JH0192.
                                                                                                                                                                                                                EMBL; X76198; CAA53791.1; -.
                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                         JACKSON F.R., NEWBY L.M., KULKARNI S.J.;
"Drosophila GABAergic systems: sequence and expression of acid decarboxylase.",
J. Neurochem. 54:1068-1078(1990).
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-i- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAD OR GLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-WOV-1995 (Rel. 32, Last annotation update)
01-MATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCE_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires
                                                                                                                                     Neurotransmitter biosynthesis; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea;
                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 SNMYSIMAARYKYFPEVKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
\vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: PYRIDOXAL PHOSPHATE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                      SNLYAFLAARHKMFPNYKE 188
                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produ-
een the Swiss Institute of Bioinformatics
SNMYAMMIARFKMFPEVKE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNMYAMMIARFKMFPEVKEK
                                              Similarity 63.2%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00392; DDC_GAD_HDC_YDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90155291
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                                                                                                 322 F
57758 MW;
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63.2%;
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                      TO GROUP II DECARBOXYLASES
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                                                                         Score
                                                                                                PYRIDOXAL P
1; 97C7A8F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRIDOXAL PHOSPHATE (POTENTIAL); 69D6C79C CRC32;
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                                                 Mismatches
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No. 7
                                                            88; DB 1; I
No. 1.07e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Decarboxylase;
                                                                                                                                     Decarboxylase;
                                                                                                                                                                                                                                                                                                     is produced through a collaboration - 
ormatics and the EMBL outstation -
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1.41e-10;
                                                                                                             PHOSPHATE (POTENTIAL).
                                                                                                                                                                                                                                                                            There are no restrictions 
ng as its content is in
                                                                                                 CRC32;
                                                                                                                                                                                                                                                     http://www.isb-sib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachycera;
                                                                       Length 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 594;
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Best Local :
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01-FEB-1994
01-FEB-1994
01-NOV-1997
LT 12

MAK_RAT

STANDARD; PRT; 622 AA
P20793;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7
ASSOCIATED KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase with a potential Differentiation 53:115-122(1993) -!- FUNCTION: COULD HAVE AN TMPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last Sequence update)
01-FCB-1994 (Rel. 35, Last annotation update)
01-MOV-1997 (Rel. 35, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S24241; S24241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLADT F., BIRCHMEIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A MEDLINE; 93366030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAK OR RCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATED KINASE) (PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAK_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:96913; MAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization and expression analysis
                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN VISUAL AND OLFACTORY SENSORY TRANSDUCTION.

IN VISUAL SAND OLFACTORY SENSORY TRANSDUCTION.

TISSUE SPECIFICITY: IN PRE- AND POSTMEIOTIC MALE GERM CELLS IN TRESTIS. IN PHOTORECEPTOR CELLS OF THE REFINA AND IN THE OLFACTORY RECEPTORS, AND IN CERTAIN EPITHELIA OF THE RESPIRATORY TRACT AND CHOROID PLEXUS (BRAIN).

DEVELOPMENTAL STAGE: ON DAY 14 OR 17 OF EMBRYONIC DEVELOPMENT.

SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THR PROTEIN KINASES. BELONGS TO THE CDC2/CDXX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: COULD HAVE AN IMPORTANT FUNCTION IN SENSORY CELLS AND IN SPERMATOGENESIS. MAY PARTICIPATE IN SIGNALING PATHWAYS USED
                                                                                                                                                                                                                                                                                                                           NLYQLMKDRNKLFPE 99
                                                                                                                                                                                                                                                                            NMYAMMIARFKMFPE
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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622 AA;
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125
125
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18
33
125
368
70050
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                                                                                                                                                                                                                                                                            16
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                                                                                                                                                                                                                                                                                                                                                                               Score 72;
Pred. No.
3; Misma
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLU/PRO-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A3D11D70 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                   on update)
(EC 2.7.1
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; I
1.36e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the murine rck gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 622;
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                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Mus.
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Matches
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Q58099;
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BINDING
ACT_SITE
DOMAIN
SEQUENCE
SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDDOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATSUSHIME H., JINNO A., TAKAGI N., SHIBUYA M.;
"A novel mammalian protein kinase gene (mak) is
testicular germ cells at and after meiosis.";
MOI. Cell. Biol. 10:2261-2268(1990).
-I- FUNCTION: COULD PLAY AN IMPORTANT FUNCTION
-I- TISSUE SPECIFICITY: EXPRESSED MAINLY IN TES
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Eukaryota;
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                                                                                                                                                                                                                                     01-NOV-1997
01-NOV-1997
                                                                                                                                                                               Methanococcus jannaschii.
Archaea; Euryarchaeota; M
                                                                                                                                                                                                                       HYPOTHETICAL
                                                                                                                                                                                                                                                                  01-NOV-1997
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DOMAIN 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Serine/threonine-protein kinase;
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ota; Metazoa; Chordata; Craniata; Vertebrata;
ia; Rodentia; Sciurognathi; Muridae; Murinae;
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PS00108; PROTEIN_KINASE_ST; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
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L PROTEIN MJ0686.
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53.3%;
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ATP (BY SIMILARITY).
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P40535;
01-FEB-1995
01-FEB-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., CHURCHER C.M., CONNOR R., COPSEY TJ., DAVIN K., FRASER GENTLES S., HAMKIN N., HORSNELL T.S., HUNT S., JAGELS K., JONES LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WALSH S.V., WHITEHEAD S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: TO YEAST YER045C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                         Hypothetical
NP_BIND 3
                                                                                                                                                                                                                                                                       EMBL; Z46861; CAA86915.1; PFAM; PF00170; bZIF; 1.
                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 5
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Science 273:1058-1073(1996).
                                                                                                                                                                                               SEQUENCE
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580 AA; 6
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587 AA; 65264 MW: 3DC
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etaceae; Saccharomyces
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(Rel. 31, Last sequence update)
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L 65.3 KD PROTEIN IN NOT3-CKA1 INT
                                                                                               Conservative
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No. 1.59e+00
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2.37e+00;
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Search completed: Tue Mar 7 21:15:47 2000 Job time : 6 secs.
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Best Local Similarity 30.0%;
Matches 6; Conservative
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MERRISON D. HOANG L. KERGLE P., LUMM W., POTHIER B., QIU D., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., JUNANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABBAKAR S., MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., MCDOUGALL S., SHIMER G., FOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C. J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                           EMBL; U47134; AAA87051.1; -.

EMBL; AE000796; AAB84553.1; -.

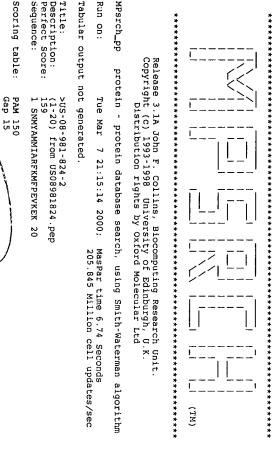
PROSITE; PS00627; GHMP_KINASES_ATP; 1.

Transferase; Kinase; ATP-binding.

NP_BIND 90 100 ATP (POTENTIAL).

CONFLICT 108 108 A -> P (IN REF. 2).

SEQUENCE 303 AA; 32224 MW; DAA8B6D9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIME_METTH STANDARD: PRT; 303 AA. Q50559; 026152; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) MEVALONATE KINASE (EC 2.7.1.36) (MK).
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MEDLINE; 98037514.
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SHARMA S., REEVE J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO OTHER SPECIES MEVALONATE KINASE.
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                                                                                                                        181 ARMVAGVAERFRRFPDIMGR 200
                                                                                1 SNMYAMMIARFKMFPEVKEK 20
                                                                                                                                                               Score 64; DB 1; Length 303; Pred. No. 3.50e+00; 7; Mismatches 7; Indels
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sequence: Description: Perfect Score: Title:

Searched

225878-seqs, 69334122 residue:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_bage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 29.459; Variance 46.484; scale 0.634

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

21188 21188	Result
152 143 143 143 118 118 1118 1112 1112 1112 1112 1112	Score
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182 13 182 13 590 13 590 13 593 13 182 13 182 13 593 13 182 13 593 13 182 13 593 13 593 13 593 13 182 13 593 13 59	Length DB
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4- i U	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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THYMOMA VIRAL PROTO-ON	SCBI2 PROTEIN.	CYTOCHROME C OXIDASE P		CYTOCHROME C OXIDASE P	CYTOCHROME C OXIDASE P	CYTOCHROME C OXIDASE P	RAB3 EFFECTOR.	CYTOCHROME P450 CYP6B9	CONSERVED HYPOTHETICAL	PROBABLE F1-F0 ASSEMBL	HYPOTHETICAL 5.7 KD PR	KINASE-LIKE PROTEIN.	HYPOTHETICAL 186.4 KD	YJDK PROTEIN.	HYPOTHETICAL 45.6 KD P	HYPOTHETICAL PROTEIN M	MINOR CAPSID PROTEIN.	YKUW PROTEIN.	HYPOTHETICAL 39.7 KD P	CONSERVED HYPOTHETICAL	GLUTAMATE DECARBOXYLAS			
1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	6.91e+00	6.91e+00	6.91e÷00	6.91e+00	6.91e+00		3.26e+00	2.23e+00	6.95e-01	6.95e-01		. 68e	3.15e-01		2.14e-03

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Q9W659 PRELIMINARY;

Q9W659;

Q1-NOV-1999 (TIEMBLrel. 12, Created)

O1-NOV-1999 (TIEMBLrel. 12, Last sequence update)

O1-NOV-1999 (TIEMBLrel. 12, Last annotation update)

O1-NOV-1999 (TIEMBLrel. 12, Last annotation update)

O1-NOV-1999 (TIEMBLIED ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
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O9W661; OF CARROLLED

O1-NOV-1999 (TEMBLrel. 12, Last sequence update)

O1-NOV-1999 (TEMBLrel. 12, Last annotation update)

O1-NOV-1999 (TEMBLREL. 12, Last annotation update)

O1-NOV-1999 (TEMBLREL. 12, Last annotation update)

O1-NOV-1999 (TEMBLREL. 12, Last sequence update)
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NON_TER
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SEQUENCE
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"Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates: molecular phylogeny and evidence for a new GAD paralog.";
Mol. Biol. Evol. 16:397-404(1999).
EMBL; AF043272; AAD22718.1;
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TISSUE-BRAIN;
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Eukaryota; Metazoa; Chordața; Craniata; Vertebrata;
Cryptodira; Testudinoidea; Emydidae; Trachemys.
                                                                                                                                                                                                                                                                         h 95.6%;
Similarity 95.0%;
19; Conservative
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182 AA;
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Pred. No. 1.86e-17;
1; Mismatches 0
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SEQUENCE
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
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                                                                                   GLUTAMATE
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Eukaryota: Metazoa: Chordata:
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PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases (
molecular phylogeny and evidence for a new GAD
mol. Biol. Evol. 16:397-404(1999).
                     Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G., PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates: molecular phylogeny and evidence for a new GAD paralog.";
mol. Biol. Evol. 16:397-404(1999).
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EMBL; AF043270; AAD22716.1;
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Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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Cyprinoidea; Cyprinidae;
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larity 85.0%;
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    Teleostei;
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  Euteleostei;
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Pred. No. 1.
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4.1.1.15) (FRAGMENT).
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Pred. No. 1
                   (Zebra dan
Craniata;
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eostei; Ostariophysi; (
ininae; Carassius.
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1. No. 1.92e-15;
Mismatches 0;
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No. 1.86e-17;
Ostariophysi; Cypriniformes;
                                        danio).
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                   Vertebrata; Actinopterygii;
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99656; PRELIMINARY;
099656;
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Coryphaenoides armatus
                        GAD67
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BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D.

PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;

"Multiplicity of glutamic acid decarboxylases (GAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coryphaenoides armatus. Eukaryota; Metazoa; Chordata;
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MARTIN S.C., HEINRICH G., SANDELL J.H.;
"Sequence and expression of glutamic acid decarbox;
the developing zebrafish.";
1. Comp. Neurol. 396:253-266(1998).
1. COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
1. COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
1. SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecular phylogeny and evidence for a new Mol. Biol. Evol. 16:397-404(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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Macrouridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                           86.8%;
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12, Last sequence update)
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ISOFORM 67 (EC 4.1.1.15) (FRAGMENT).
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ISOFORM 65 (EC 4.1.1.15) (F
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                                                                                                                                                                                                                                                                            57
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                                                                                                                                                                                                                                                                                                                     Pred.
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Pred. No. 1.92e-15;
                                                                                                                                                                                                                                                                                                                                           Score 138;
Pred. No.
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GLUTAMATE DE
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Macrouridae;
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Q9W655;
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"Multiplicity of glutamic acid decarboxylases (GAD) molecular phylogeny and evidence for a new GAD paral Mol. Biol. Evol. 16:397-404(1999).
EMBL; AF043268; AAD22714.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP TRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases (
molecular phylogeny and evidence for a new GAD
MOL Biol. Evol. 16:397-404(1999).
EMBL; AF043266; AAD22712.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
GLUTAMATE DECARBOXYLASE ISOFORM 67 (EC 4.1.1.15) (FRAGMENT).
      Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carassius auratus (Goldfish).
Eukaryota: Metazoa; Chordata;
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larity 75.0%;
Conservative
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Teleostei; Eutelo
Coryphaenoides.
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19851 MW;
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(EC 4.1.1.15) (FRAGMENT).
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Pred. No. 5.15e-10;
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Pred. No. 1.01e-11;
3; Mismatches 2
   (Zebra danio)
Craniata; Ver
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      Vertebrata;
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                       GAD67
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"Multiplicity of glutamic acid decarboxylases (GAD) in molecular phylogeny and evidence for a new GAD paralog. Mol. Biol. Evol. 16:397-404(1999).
EMBL; AF043271; AAD22717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poephila guttata (Zebra finch) (Taeniopygia guttata).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; /
Neognathae; Passeriformes; Estrildidae; Estrildinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYRDC).

EMBL; AF017266; AAC24327.1; -
PROSITE; PS00392; DDC_GAD_HDC_YDC;
PROSITE; PS00392; DVT1doxal_deC; 1.
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"Sequence and expression of glutamic acid decarboxy
the developing zebrafish.";
J. Comp. Neurol. 396:253-266(1998).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
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                                           GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 98295903.
Pseudemys scripta
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                                                                                                                                                                                                                                                                       <u>8</u>
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Similarity 70.0%;
14; Conservative
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Similarity 70.0%;
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99 (TrEMBLrel. 12, Last annotation update)
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; Rasborinae; Danio.
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                                    Last sequence update)
Last annotation update)
PFORM 67 (EC 4.1.1.15) (F
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Pred. No. 5.15e-10;
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1. No. 9.32e-09;
Mismatches 3;
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Q9Y158;
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01-NOV-1996
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"Multiplicity of glutamic acid decarboxylases (GAD) in molecular phylogeny and evidence for a new GAD paralog. Mol. Biol. Evol. 18:397-404(1999).

EMBL; AF043274; AAD22720.1; -.
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PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_dec; 1.
Lyase; Decarboxylase; Pyridoxal phosphate.
SEQUENCE 563 AA; 64095 MW; CBBBOC98 CF
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                                          Neognathae;
                                                                                                                                                             Gallus gallus (Chicken).
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
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Cryptodira;
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Pred. No. 9.32e-09;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 112; DB 13;
Pred. No. 9.32e-09;
                                                                                                                   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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II DECARBOXYLASES (DDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           590 AA
                                                                                 Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local Similarity
Watches 14; Conserv
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09W658;

01-NOV-1999

01-NOV-1999

01-NOV-1999
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008685
008685;
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"Characterization of glutamate decarboxylase in cl
"Characterization of glutamate decarboxylase in cl
submitted (OCT-1997) to tha EMBL/GenBank/DDBJ data
-i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)
-i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASE
MEDLINE; 99261650.

BOSMA P.T., BLAZQUEZ M., C
PRIEDE I.G., DOCHERTY K.,
"Multiplicity of glutamic
                                                                                                                                                                                                                                                                                                                                                              GAD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y17257; CAA72934.1; --
PROSITE; PS00392; DDC_GAD_HDC_YDC;
PFAM; PF00282; Pyridoxal_deC; 1.
Lyase; Decarboxylase; Pyridoxal pho
SEQUENCE 593 AA; 66648 MW; BAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
67KD GLUTAMIC ACID DECARBOXYLASE.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                          Coryphaenoides armatus.
Eukaryota: Metazoa: Cho
                                                                                                                                                                                                                                                                                                                                                                                        GLUTAMATE DECARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1997) to -!- COFACTOR: PYRIDOXAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C;
AUST G., STEINBRENNER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00392; DDC_GAD_HDC_YDC;
Lyase; Decarboxylase; Pyridoxal pho
SEQUENCE 590 AA; 66710 MW; 80Bf
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                     TISSUE=BRAIN
                                                                                                                                                                                                                         Macrouridae; Coryphaenoides.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.)
(TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                   Teleostei;
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70.0%;
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70.08;
                                                                                                                                                                                                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Ver
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the EMBL/GenBank/DDBJ databases.
PHOSPHATE (BY SIMILARITY).
TO GROUP II DECAPROVO....
                                                                                                                                                                                                                                                                                                                                                                        12, Created)
12, Last sequence update)
12, Last annotation update)
13, Last annotation update)
15OFORM 3 (EC 4.1.1.15) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO GROUP II DECARBOXYLASES
                                                                                                                                                                                                                                                             Euteleostei;
                                          COLLINS M.A., BISHOP, TRUDEAU V.L.;
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            acid decarboxylases
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Pred. No. 9.32e-09;
3; Mismatches 3
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Pred. No. 9.32e-09;
3; Mismatches 3
                                                                                                                                                                                                                                                         Craniata; Vertebrata; Actinopterygii; sostei; Paracanthopterygii; Gadiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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ae; Murinae;
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J databases
                                                                    J.D.D.,
            (GAD)
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Mus.
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            vertebrates:
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Search completed: Tue Mar Job time: 9 secs.
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                                                                                                                                                                                                                                            Query Match 57.2%; Score 91; DB 11; Let Best Local Similarity 50.0%; Pred. No. 1.54e-04; Matches 10; Conservative 6; Mismatches 4;
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SEQUENCE
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EMBL; M64755; AAC42063.1; -.

PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_dec; 1.

Lyase; Decarboxylase; Pyridoxal phosphate.

SEQUENCE 478 AA: 53725 MW; 4CAC0093 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         decarboxylase.";
Blochim. Blophys. Acta 1262:79-82(1995).
-I- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).
-I- COFACTOR: PYRIDOXAL-PHOSPHATE.
-I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1996 (TIEMBLIEL 12, Last annotation update)
CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)
(SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
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KAISAKIA P.J., JERKINS A.A., GOODSPEED D.C., STEELE R.D.;

"Cloning and characterization of rat cysteine sulfinic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular phylogeny and evidence for a new GAD paralog."; Mol. Biol. Evol. 16:397-404(1999).
EMBL; AF043269; AAD22715.1; -.
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STRAIN-SPRAGUE-DAWLEY;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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23-SEP-1991; 006872.
21-SEP-1990; US-586536.
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DE19526561-A1.
23-JAN=1997.
prods.
Sequence
                             therapeutic and diagnostic application in insulin-dependent diabetes mellitus patients
Disclosure; Fig 3; 53pp; English.
The sequence given is a glutamic acid decarboxylase (GAD65). GAD65 can be used for the diagnosis and therapy of patients with autoimmune diseases, esp insulin-dependant diabetes mellitus (IDDM) and "stiff man" syndrome. It is possible to use either the entire GAD65 protein or polypeptide fragments of it for the immunological detection of autoantibodies to GAD65 which are indicative of IDDM and other auto-immune diseases. The production of this sequence by recombinant DNA technology allows large scale production of eukaryotic GAD65 in its native from without the need for separation form other proteinaceous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 11; Page 9; 12pp; German.

W18842-70 are peptide fragments of the 65 kD human glutamic acid decarboxylase (GAD). The fragments are autoreactive substances used for diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is determined by using a claimed method for diagnosis of cell-mediated diseases or a predisposition to cell-mediated diseases, which is effected by administering an autoreactive substance intradermally and establishing the diagnosis on the basis of the occurrence or lack of a positive reaction at the site of administration. The method is used for diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated diseases such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 kD Glutamic acid decarboxylase peptide fragment III. GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis; insulin-dependent diabetes mellitus; IDDM; cell-mediated disease; predisposition_autoimmune; tumour; rheumatoid arthritis; multiple_Sclerosis
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Donie F, Endl J, Gar
Pozzilli P, Stahl P;
WPI; 97-088254/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skin test for diagnosis of cell-mediated diseases, esp. diabetes involving intradermal admin. of auto:reactive substances
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20-JUL-1995; DE-026561
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02-DEC-1993; US-984935.
03-DEC-1992; US-984935.
(REGC ) UNIV CALLFORNIA.
Baekkeskov S, Kim J, Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New soluble fragments of glutamic acid decarboxylase protein used for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome. Disclosure: Fig. 1; 73pp; English syndrome. The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletions full timit solubility. Different fragments contain epitopes for different classes of GAD65 autoantibodies.
or MICA2. These mutants also have some N-terminal modifications to improve solubility. Sequence 544 AA;
                                                                           Disclosure; Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and (R59517) were determined. New soluble fragments of G (R59518-25) were prepared by deletion/substitution mutagenesis. The C-terminally deleted mutants given are able to recognize IDM autoantibodies having the of MICA4/MICA6, but not those having the specificity
                                                                                                                                                                                                                                                                         New soluble fragments of glutamic acid decarboxylase used for the diagnosis and treatment of insulin dependiabetes mellitus and stiff man syndrome.
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GAD65; glutamate-decarboxylase; diabetes mellitus;
stiff man syndrome; autoantibody; mutagenesis.
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WPI; 94-200193/24.
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W09412529-A.
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R59524;
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glutamate-decarboxylase; diabetes mellitus;
man syndrome; autoantibody; mutagenesis.
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No. 1.92e-08;
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                                                                                                                                                                                              GAD65
                                                                                   of MICA1/MICA3
                                                                                                          specificity
                                                                                                                                          in R59524-25
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Matches 2
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25-MAY-1995; 450755.
02-DEC-1993; US-161290.
03-DEC-1993; US-984935.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
(REGC ) UNIV CALIFORNIA.
Backkeskov S, Kim J, Namchuk M, Richter W,
WPI; 99-089720/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-1994.
02-DEC-1993; U11705.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
Baekkeskov S, Kim J, Na
diabetes and stiff man syndrome
Examples: Fig 1; 31pp; English.

This represents a human GAD65 protein sequence. The invention provides soluble fragments of GAD65 that are specifically reactive with at least one class of GAD65 autoantibody. The fragments are substantially free of N-terminal amino acids that would otherwise limit solubility. Different fragments contain different epitopes for different classes of GAD65 autoantibodies. These fragments are used in the methods of the invention for detection of GAD65 autoantibodies. The methods are used for monitoring insulin-dependent diabetes mellitus (IDDM) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 94-200193/24.

We soluble fragments of glutamic acid decarboxylase protein used for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome.

Disclosure: Fig. 1: 73pp: English.

Disclosure: Fig. 1: 73pp: English.

GR59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for sequence 554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 6
R59518;
R59518;
                                                                                                                                                                                                                                                                                   Human GAD65 protein sequence.
GAD65; autoantibody; soluble; detection; diagnosis; monitor;
insulin-dependent diabetes mellitus; stiff man syndrome.
                                                                                                                                                                                                                                                                                                                                                              T 7
W86017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stiff man syndrome; autoantibody; mutagenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
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Similarity 100.0%;
20; Conservative
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Similarity 100.0%;
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Pred. No. 1.92e-08;
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Pred. No. 1.92e-08
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Best Local Similarity 100.0%;
Matches 20; Conservative
WO9700891-A1.
09-JAN-1997.
24-JUN-1995; US-494624.
23-JUN-1995; US-494624.
(KENN-) KENNEDY INST RHEUMATOLOGY.
(KEUR-) NEUROCRINE BIOSCIENCES INC.
(SBAR-) ST BARTHOLOMEM'S HOSPITAL C
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US5691448-A.
25-NOV-1997.
                                                                                                                                                                                          W12402;
08-0CT-1997 (first entry)
65 kD human glutamic acid decarboxylase isoform.
65 kD glutamic acid decarboxylase; human; GAD65;
neuron; central nervous system; type I diabetes;
T_cell; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stiff-man syndrome Disclosure; column 27-30; 30pp; English.

This sequence represents the human glutamic acid decarboxylase protein This sequence represents the human glutamic acid decarboxylase protein GAD65. The invention relates to soluble fragments of a GAD65 protein that are specifically reactive with a GAD65 autoantibody (AAb), where the fragment is at least 99% pure and the AAb binds to a conformational epitope of the fragment. The soluble GAD65 fragments can be used to distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff man syndrome. They can also be used for diagnosis and treatment of IDDM and stiff man syndrome. The fragments can distinguish different temporal stages in the progression of IDDM.

Sequence 584 AA;
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W34519
W34519;
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02-DEC-1993; US-161290.
03-DEC-1992; US-984935.
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GAD65; glut
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Sequence 584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble fragments of glutamic acid decarboxylase distinguish between insulin-dependent diabetes me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baekkeskov S, Kim WPI; 98-017711/02.
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          W12402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NWELADOPONLEEILMHCOT
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                          Protein; 585
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     HOSPITAL CENT CLINICAL.
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Pred. No. 1.92e-08;
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Pred. No. 1.
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L.92e-08;
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                                                                                                                                                                                                                               enzyme; pancreas;
autoimmune respon
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IDDM; diagnosis;
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This sequence represents the 65 kD isoform of human glutamic acid decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of the pancreas, and in neurons of the central nervous system. There are two isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of GAD65 have been identified in Type I diabetic patients. Fragments of GAD65, and analogues of the fragments, are used in the methods of the GAD65, and analogues of the fragments, are used in the methods of the invention. The methods are for detecting or treating diabetes or a predisposition to diabetes. The peptides can also be used for ameliorating an autoimmune response in a patient. Alteration of the native peptides with selective changes of crucial residues can induce unresponsiveness or change the responsiveness of antigen-specific and do not cause proliferation of the corresponding native beptide-specific T cells. The peptide analogues compete for binding to MHC sequence 585 AA;
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Matches
     Matches
                                     Query Match
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                                                                                                                                                                                                               Claim 3; Page 13-15; 24pp; English.

A modified human glutamic acid decarboxylase (GAD) (W14915) has the native lysine residue at amino acid position 39 replaced by arginine. It is obtd. by site-directed mutagenesis (see also T64561) of native human GAD65 cDNA and expression of the mutant DNA (T64560) in transformed host cells. Lys-396 is critical for enzyme activity. By replacing it with an amino acid incapable of Sthiff
                                                                                                          disorders such as insulin-dependent diabetes mellitus (IDDM) and other diseases, e.g. neurological diseases, esp. in individuals having a genetic predisposition for IDDM or with an increased
                                                                           having a genetic predisposition antibody titre against GAD. Sequence 585 AA;
                                                                                                                                                                                                         base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme engineering;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified glutamic acid decarboxylase (K396R). Glutamic acid decarboxylase; GAD; autoimmune disease; therapy; indulin-dependent diabetes mellitus; vaccine;
                                                                                                                                                                 is reduced or lost, so minimising the risk of toxicity. The modified GAD can be used to treat and/or prevent autoimmune
                                                                                                                                                                                                                                                                                                                                                                       enzyme activity, esp.
                                                                                                                                                                                                                                                                                                                                                                        Modified glutamic acid decarboxylase for autoimmune disease treatment - has immunoreactivity of unmodified GAD65 but denzyme activity, esp. useful for insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-212895/19.
N-PSDB; T64560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNE-) SYNECTICS BIOTECHNOLOGY AB.
Essen-Moeller A, Falorni A, Lernn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-1996; SE1210.
29-SEP-1995; SE-003379
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                                                                                                                                                                                                                                                                                                                                                         treatment
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                    Local
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                                                                                                                                                                                                         formation,
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100.0%;
Similarity 100.0%;
20; Conservation
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20; Conservative
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determining predisposition
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 Score 154; DB 1;
Pred. No. 1.92e-08;
0; Mismatches (
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Pred. No. 1.92e-08;
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Best Local
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15-MAY-1991; US-702162.
(UNIW) UNIV WASHLIGTON.
(ZYMO) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by giving Ga
                                                                                                                                                 Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y; WPI; 94-200193/24.

New Soluble fragments of glutamic acid decarboxylase protein used for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome.

Disclosure; Fig. 1: 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution
that limit solubility. Different fragmen different classes of GAD65 autoantibodies Sequence 585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1994.
02-DEC-1993; U11705.
03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAD65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin dependent diabetes mellitus
Disclosure; Fig 2; 45pp; English.
The sequence is that of human pancreatic islet glutamic acid
decarboxylase (GAD) which is used to test biological samples for
the presence of autoantibodies to human GAD. It can also be used
to remove antibodies against GAD from plasma in order to treat an
autoimmune response to GAD, e.g. in insulin-dependent diabetes melting
(IDDM), and may also be used to induce immunological tolerance to GAD
by giving GAD that specifically binds the GAD receptor on immature T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster DC, Grubin CE, Hagopian W, Karlsen AE, Lernmark A, OHara WPI; 92\text{-}415789/50. N-PSDB; Q31783.
                                                                                                                        mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
WO9412529-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stiff man syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R59516
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Human pancreatic islet cell glutamic acid decarboxylase.
GAD; insulin dependent diabetes melting; IDDM; autoantibody detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GAD65
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hes 20; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamate-decarboxylase; diabetes mellitus;
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                                                                           These fragments are free of N-terminal amino acids lubility. Different fragments contain epitopes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoantibody.
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Query Match 100.0%; Best Local Similarity 100.0%;

> Score 154; DB 1; Pred. No. 1.92e-08

Length 585

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24-AUG-1994; U09478.
17-SEP-1993; US-123859.
(REGC) UNIV CALIFORNIA.
Clare-Salzler MJ, Erlander MC
WPI: 95-131360/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide fragments of glutamic acid decarboxylase - for diagnosis and treatment of auto: immune disease, esp. insulin dependent diabetes, also related nucleic acid, vectors, antibodies, hybridoma(s) etc.

Example 1; Fig 3: 10bp; English.

Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic acid decarboxylase (GAD65) respectively, from which the GAD65 fragments described in R72561-R72298 were derived. These fragments can be used to detect autoantibodies against GAD, e.g. to diagnose and treat GAD-related autoimmune disorders, such as insulin dependant diabetes mellitus or stiff man disease.

Sequence 585 AA;
                                                                                                                                                                                                   03-APR-1997.
03-APR-1996; SE1210.
29-SEP-1995; SE-003379.
(SYNE-) SYNECTICS BIOTECHNOLOGY AB.
(SYNE-) SYNECTICS BIOTECHNOLOGY AB.
ESSEN-Mocller A, Falorni A, Lernmark A,
WPI; 97-212895/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R79105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified glutamic acid decarboxylase. GAD: autoimmune Glutamic acid decarboxylase; GAD: autoimmune indulin-dependent diabetes mellitus; vaccine;
                    Claim 1; Page 16-18; 24pp; English.

A modified human glutamic acid decarboxylase (GAD)
native Lys residue at amino acid position 396 repla
His, Gly or esp. Arg (see also W14915). It is obto
                                                                                                                                  Modified glutamic acid decarboxylase for autoimmune disease treatment - has immunoreactivity of unmodified GAD65 but duenzyme activity, esp. useful for insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1995 (first entry)
Human glutamic acid decarboxylase (GAD65).
Rat glutamic acid decarboxylase; GAD65; auotimmune disorders;
insulin-dependant diabetes mellitus; stiff man disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W14916;
10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                              WO9712034-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W14916 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%;
Similarity 100.0%;
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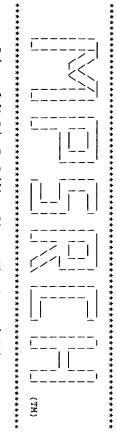
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16-MAR-1995.
02-SEP-1994; U09937.
07-SEP-1993; US-117907.
(UNIW ) UNIV WASHINGTON.
(UNIW ) KAILSEN AE,
                                                                                                                                                                                                                                          decarboxylase.

Claim 8: Page 40-44; 62pp; English.

A human islet cDNA library was screened for colonies containing GAD cDNA using probes (given in Q86047-49) based on conserved internal and N- and C-terminal regions of cat, rat and mouse brackers and series obtained by PCR-RACE. The entire GAD. Full-length clones were obtained by PCR-RACE. The entire sequence of the human islet GAD cDNA is given in Q86046 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R71641 stand
R71641;
21-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting the clinical course of diabetes in patients winon-insulin dependent diabetes mellitus - by detecting the presence of auto:antibodies to human islet cell glutamic
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WPI; 95-123
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                                                                                                                                                                                                                   Sequence
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:25:58 2000; MasPar time 4.71 Seconds 200.441 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-981-824-3 (1-20) from US08981824.pep 154

1 NWELADQPQNLEEILMHCQT 20

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 29.232; Variance 44.473; scale 0.657

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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<pre>NMD5 protein - yeast gag-pro-pol polyprote</pre>	zeaxanthin epoxidase	xanthophyll epoxidase	flagellar hook-associ	microtubule-associate	condensin XCAP-D2 cha	kinesin-associated pr	٠.	arylsulfatase E (EC 3	probable membrane pro	methylated-DNAprote	posterior-group prote	probable allene oxide	hypothetical 61.6 kD	cell adhesion protein	conserved hypothetica	×		hypothetical protein	DNA repair protein ra	ribosomal protein L17
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ALIGNMENTS

RESULT 2 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors	Ouery Match Best Local Sim. Matches 20; Matches 146 NWELADO Db 146 NWELADO Qy 1 NWELADO	CLASSIFICATION KEYWORDS FEATURE 393-396 SUMMARY	#accession JC4064 #accession JC4064 ##molecule_type mRNA ##residues 1-58 ##cross-references D ##cross-references D ##experimental_sourc COMMENT This enzyme cathooks	ACCESSIONS REFERENCE #authors #journal #title	RESULT 1 ENTRY TITLE ORGANISM DATE
A41292 #type complete glutamate decarboxylase (EC 4.1.1.15) 2 - human glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Homo sapiens #common_name man 13-May-1992 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999 A41935; A41292; S30058; B54778 A41935 Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;	tch 100.0%; Score 154; DB 2; Length 585; al Similarity 100.0%; Pred. No. 5.28e-19; 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; NWELADQPQNLEEILMHCQT 165	w #superfamily human glutamate decarboxylase N carbon-carbon lyase; carboxy-lyase #domain DOPA decarboxylase binding #status predicted #label BIN #length 585 #molecular-weight 65388 #checksum 5933	#accession JC4064 #accession JC4064 ##molecule_type mRNA ##residues 1-585 ##label SUZ ##cross-references DDJ:D31848; NID:g790964; PIDN:BAA06635.1; #ID:g790965 ##experimental_source brain ##experimental_source brain ##experimental_source catalyzes the conversion of glutamic acid into	JC4064 JC4064 SUZUKI, R.; Asami, N.; Amann, E.; Wagatsuma, M. Suzuki, P.; Asami, N.; Amann, E.; Wagatsuma, M. Gene (1995) 152:257-260 Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).	JC4064 #type complete glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig #format_name Sus scrofa domestica #common_name domestic pig 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 22-Jun-1999

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#contents annotation; intron-exon boundaries

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic aci
it has several isoforms, each encoded by a separate gene. GAI
also been implicated as an autoantigen in autoimmune disease
                                                                                                                                                                                                                                                FEATURE
396
                                                                                                                                                                                                                                                                                                                ##cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phospho
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#journal Eur. J. Biochem. (1993) 212:597-603

#title Characterization of a linear epitope within the human pancreatic 64-Kba glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.
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Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes,
Grant, F.J.; Foster, D.; Lernmark, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.
#cross-references MUID:92020848
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##cross-references EMBL:X69936
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\vdash
NWELADOPQNLEEILMHCQT
                                                                                        100.0%;
Similarity 100.0%;
20; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stiff-man syndrome and insulin-dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bu, D.F.; Tobin, A.J. Genomics (1994) 21:222-228 Genomics (1994) 21:222-228 The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                     GDB:GAD2
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Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
                                                                                                                                                                                              #length
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                                                                                                                                                                                                                                                                                           phosphate
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h 585 #n
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                                                                                                                                                                                      us predicted
#molecular-weight 65411
20
                                                                                                                    Score 154; DB 1;
Pred. No. 5.28e-19;
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                                                                                                                                           Length 585;
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*authors Chang, Y.C.; Gottlieb, D.I.

#journal J. Neurosci. (1988) 8:2123-2130

#title Characterization of the proteins purified wi

#title antibodies to glutamic acid decarboxylase.

#cross-references_MUID:88258610
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                                                                                #cross-references MUID:94032481
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'V,191-194,'X',196-203,'XX',206-219;'X',225-234,'X',
236-247,'X',249-266,'X';524-537,539-543,'V',547-549,
'X',551-553,'X',555-558 ##label CHA

NT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.

IFICATION #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 NWELADQPQNLEEILTHCQT 165
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##molecule_type mRNA
##residues 1-58
                                          ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NWELADOPONLEEILMHCQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                              $38533 #type complete
glutamate decarboxylase (EC 4.1.1.15) 2 - mouse
glutamate decarboxylase (BAD65; L-glutamate 1-carboxy-lyase
glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
#formal_name Mus musculus #common_name house mouse
#formal_name Mus musculus #common_name house mouse
20-May-1994 #sequence_revision 23-Mar-1995 #text_change
                                                                                                                                                                                            S38533
S38533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
#length 585 #molecular-weight 65402 #charton.... 7757
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glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
#formal_name Rattus norvegicus #common_name Norway rat
31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change
                                                                                                     Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L. Biochim. Biophys. Acta (1993) 1216:157-160 Cloning and sequence analysis of a murine cDNA glutamate decarboxylase (GAD65).
                                                                 S38533
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Neuron (1991) 7:91-100
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His, TCA for residue 198 as Ala, and CAG
1-585 ##label LEE
                                          preliminary
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95.0%;
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Pred. No. 3.27e-16;
0; Mismatches 1;
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#accession I59173
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NT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
thas several isoforms, each encoded by a separate gene.
If ICATION #superfamily human glutamate decarboxylase
RDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                ##experimental_source brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 ELSDHPESLEQILVDCR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-223 ##label RES
##cross-references GB:M38350; NID:g204231; PIDN:AAA41185.1;
#FICATION #superfamily human glutamate decarboxylase
#Y #length 223 #molecular-weight 25069 #checksum
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                                                                                  ##residues 1-585 ##label
##cross-references EMBL:Z49976
                                                                                                   ##residues
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submitted s
561533
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Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775
Developmentally regulated expression of an exon of
stop codon in the gene for glutamic acid decarbo
                                                                                                                                       S61534
                                                                                                                                                                    Katarova, Z.; Szabo, G.; Mugnaini, E.
Eur. J. Neurosci. (1990) 2:190-202
Molecular identification of the 62 kd
                                                                                                                                                                                                                                            S61534; S61533
                                                                                                                                                                                                                                                          #formal_name Mus musculus #common_name house mouse 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_c 22-Jun-1999
                                                                                                                                                                                                                                                                                                           glutamate decarboxylase (EC 4.1.1.15)
glutamic acid decarboxylase
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#formal_name Rattus norvegicus
02-Jul-1996 #sequence_revision
                                    Szabo, G.
                                                    S61533
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                                                                                                                                                       decarboxylase from the
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#status predicted
#th 585 #molecular-weight 65224 #checksum 7599
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Pred. No. 4.02e-04;
7; Mismatches 1
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Pred. No. 3.27e-16;
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#accession JH0195

##molecule_type mRNA
##melecule_type mRNA
##residues 1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',
##residues 1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',
##cross-references GB:X57572; NID:956185; PIDN:CAA40800.1; PID:956186

MMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.

LASSIFICATION #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxa
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Best Local
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#journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                  ##status preliminary
##molecule_type mRNA
1-593 ##label WYB
##rcross-references GB:X57573; NID:g56183; PIDN:CAA40801.1;
##cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1;
##note the authors translated the codon TGT for re
##note Ser and TCT for residue 413 as Cys
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##residner
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PID:g886687
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glutamate decarboxylase (EC 4.1.1.15) 1 - rat
glutamate decarboxylase (AD67; L-glutamate 1-carboxy-lyase
#formal_name Rattus norvegicus #common_name Norway rat
12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
                                                                                                                                                                                                                                                                               Julien, J.F.; Samama, P.; Mallet, J.
J. Neurochem. (1990) 54:703-705
Rat brain glutamic acid decarboxylase sequence deduced cloned cDNA.
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carbon-carbon lyase; carboxy-lyase
#length 585 #molecular-weight 65381 #checksum
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Dyrberg, T.; Madsen, O.D.
Proc. Natl. Acad. Sci. U.S.A.
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Pred. No. 4.02e-04;
7; Mismatches 1
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##cross references EMBL:Z22706
IFICATION #superfamily human glutamate decarboxylase
RDS carbon carbon lyase; carboxy-lyase
RDS #length 593 #molecular-weight 66952 #chec
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##residner
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##cross-references EMBL:Z22750
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Similarity 52.9%;
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Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.
Ann. Hum. Genet. (1992) 56:255-265
Nucleotide sequence and Chromosomal assignment of a
encoding the large isoform of human glutamate
                                                                                                                                                                                                                                                                          Johnstone, A. submitted to the EMBL Data Library, May S51776
                                                                                                                                                                                                                                                                                                                                                                       $$1776. #type complete
glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo sapiens #common_name man
15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
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#title Two human glutamate decarboxylases, 65 kDa GAD and
GAD, are each encoded by a single gene.
#cross-references MUII:92196068
#accession B41935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Yamashita, K.; Cram, D.S.; Harrison, L.C.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title Molecular cloning of full-length glutamic acid deca
#toss-references MUID:93282844
#cross-references MUID:93282844
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##experimental_source brain cession PQ0158
                                                                               ##molecule_type mRNA
##residues 218-
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##cross-references GB:S61897; NID:g385450; PIDN:AAB26937.1; PID:g385
##experimental_source pancreatic islet
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##experimental_source pancreatic islet
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                                                    ##cross-references GB:M70434
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Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.
Blochem. Biophys. Res. Commun. (1991) 176:1239-1244

Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawasaki, E.; Moriuchi, R.; Watanabe, M.; Saitoh, K.; Cha
Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;
Akazawa, S.; Miyamoto, T.; Nagataki, S.
Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
Cloning and expression of large isoform of glutamic acid
decarboxylase from human pancreatic islet.
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glutamate decarboxylase (EC 4.1.1.15) 1 - human
glutamate decarboxylase (AD67; L-glutamate 1-carboxy-lyase
#formal_name Homo sapiens #common_name man
31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
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B41935; JH0805; JH0806; A61406; PQ0157; PQ0158; B41367;
A36463; A54778
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Lancet (1991) 338:1468-1469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         decarboxylase
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                                                                                  218-463 ##label CR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence extracted from NCBI backbone (NCBIP:88006)
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COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic aci it has several isoforms, each encoded by a separate gene. GAD also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.
                                                             ACCESSIONS
REFERENCE
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##residues 527-594 ##label PER
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##residues 218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,

'D',331-338,'L',340-390,'S',392-397 ##label CR2

##cross-references GB:M70435; NID:g182941; PIDN:AAA52513.1; PID:g182942
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Local Similarity 52.9%;
hes 9; Conservative
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Genomics (1994) 21:272-228
The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestra
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Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758

Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent
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                                                                                                                        JC4065 #type complete
glutamate decarboxylase (EC 4.1.1.15) 67K chain - pig
#formal_name Sus scrofa domestica #common_name domestic
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
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Suzuki, R.; Asami, N.; a
Gene (1995) 152:257-260
Sequences of two porcino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #submission
                  authors
                                            ##molecule_type mRNA
##residues 1-594 ##label
##cross-references GB:M18629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
##residues 1-594 ##label JOH
##cross-references EMBL:Z22750; NID:g298098; PIDN:CAA80435.1;
##CICATION #Superfamily human glutamate decarboxylase
UDS carbon-carbon lyase; carboxy-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 ELSDHPESLEQILVDCR 173
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PID:d1007208; PID:g790967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues 1-594 ##label SUZ
                                                                                                                                                                                                                                                                                                                                                                157 ELSDHPESLEQILVDCR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 55.8%;
Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                  3 ELADOPONLEEILMHCQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This enzyme catalyzes the conversion of glutamic acid gamma-amino butyric acid.
FION #superfamily human glutamate decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $51775 #type complete
glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo sapiens #common_name man
15.7ul-1995 #sequence_revision 21.7ul-1995 #text_change
22.7un-1999
                                                                                                                                                                             glutamate decarboxylase (EC 4.1.1.15) 1 - cat
glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
#formal_name Felis silvestris catus #common_name domestic c
31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-un-1999
Kobayashi, Y.; Kaufman, D.L.; To J. Neurosci. (1987) 7:2768-2772
                              A45671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, May \$51775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S51775
S51775
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#label BIN
#length 594 #molecular-weight 66894 #checksum 5491
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                                                                                                               submitted to
                                                                                                                                               A46758; A45671
A46758
                                                                                                                                Kobayashi, Y.; Kaufman,
                                                                                                                                                                                                                                                                 A46758
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                                                                                                                                                                                                                                                                 #type complete
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                                                                                                                 GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 2;
Pred. No. 4.02e-04
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Score 85; DB 2; I
Pred. No. 4.02e-04;
                                                 KOB
NID:g163858; PIDN:AAA51430.1;
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                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                               n, D.L.; Tobin,
September 1989
                 Tobin, A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66973 #checksum
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TITLE
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REFERENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Lingueglia, E.; Champigny, G.; Lazdunski, M.; Barbry, P. #journal Nature (1995) 378:730-733 
#title Cloning of the amiloride-sensitive FMRFamide peptide-gated 
#cross-references MUID:96107314
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134,196,303,349,
365,372,473
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||:|:|:||:||: |:
3 ELADQPQNLEEILMHCQ 19
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This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
##molecule_type mRNA
1-558,'RGTRPTFSGWSSRTQLLHSPILTSSSRR' ##label KO2
##residues 1-558,'RGTRPTFSGWSSRTQLLHSPILTSSSRR' ##label KO2
                                                                                                                                                                                                                                      175 SHNLEDMLMHCR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-625 ##label LIN ##residues 1-625 ##label LIN ##cross-references EMBL:X92113; NID:g1149510; PID:e205469; PID:g1149511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
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Local Similarity 52.9%;
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Local Similarity 58.3%;
nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                      predicted #length 625 #mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein; sodium channel; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S68434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMRFamide-activated sodium channel protein, amiloride-sensitive - brown garden snail #formal_name Helix aspersa #common_name brown garden snail 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                     T14159 #type complete
protein P140 - mouse
#formal_name Mus musculus #common_name house
20.Sep-1999 #sequence_revision 20.Sep-1999 #t
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                                     20-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain transmembrane #status predicted #domain transmembrane #status predicted
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#status predicted
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Pred. No. 1.13e-01;
5; Mismatches 0
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7; N
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                                                 #text_change
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#label TM2\
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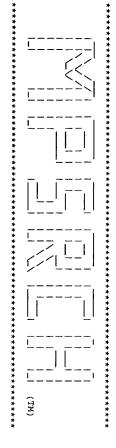
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Search completed: Tue Mar Job time : 8 secs.
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                                                                                                                                                                                                               SUMMARY
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                                                                                                                                           Matches
                                                                                                                                                        Query Match 42.9%;
Best Local Similarity 37.5%;
                                                                                                                                                                                                                                                                                                                                                       #submission #accession
                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                                                                                                                                                               ##status
##molecule_type mRNA
##mosidues 1-1216 ##label CRO
##residues 1-1216 ##label CRO
##cross-references EMBL:AF040944; NID:g3098417; PID:g3098418;
##cross-references PIDN:AAC13635.1
                                                                                                    834 LKEEPORLDGLLKRCR 849
                                                                     4 LADQPQNLEEILMHCQ 19
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                                                                                                                                                                                              P140
#length 1216 #molecular-weight 130768 #checksum 9690
                                                                                                                                       Conservative
                  7 21:26:06 2000
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Pred. No. 1.91e+00;
7; Mismatches 7
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:23:40 2000; MasPar time 3.50 Seconds 170.742 Million cell updates/sec

Tabular output not generated.

Scoring table: Sequence: Description: Perfect Score: РАМ 150 Gap 15 154 1 NWELADQPQNLEEILMHCQT 20 >US-08-981-824-3 (1-20) from US08981824.pep

Title:

Searched: Database: Post-processing: Min'imum Match 08 Listing first 45 summaries swiss-prot38 1:swissprot 82229 seqs, 29864866 residues

Statistics Mean-29..965;- Variance 40.389; scale 0.742

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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TEI	HYPOTHETICAL 61.6 KD P	POLY / 3 - HYDROXYALKANOAT	ASE	HYPOTHETICAL 54.5 KD P	DNA REPAIR PROTEIN RAD	ŲΙ	P2 PROTEIN.	VARIANT SURFACE GLYCOP	Þ	VEGETATIBLE INCOMPATIB		FMRFAMIDE-ACTIVATED AM	D-AMINO ACID OXIDASE (GLUTAMATE DECARBOXYLAS		GLUTAMATE DECARBOXYLAS	GLUTAMATE DECARBOXYLAS	Description						
	3.01e+00	,	۰			. 9	1.31e+00		. 31	7 e	. 57	. 47	.4.	.77e	. 77	.77e	.77e	.77e-0	.53e-		.14e-	1.14e-21	Pred. No.	

Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative

Score 154; DB 1; Le Pred. No. 1.14e-21; 0; Mismatches 0;

Length 585; Indels

0;

Gaps

0

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24
58	58	58	5 8	58	58	59	59	59	59	60	60	60	60	60	60	60	60	61	61	61	61
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SRF1_BACSU	MT10_YEAST	ITA8_HUMAN	STA4_MOUSE	LCK_CHICK	POTF_ECOLI	CCAH_HUMAN	OXDD_BOVIN	CG12_HUMAN	HOLB_BACSU	NMD5_YEAST	ABA2_NICPL	ABA2_CAPAN	FLGK_BORBU	RNH1_CRIFA	UL32_HSV6U	LCK_AEDAE	YAED_HAEIN	ABA2_LYCES	ARSE_HUMAN	YIT2_YEAST	MGMT_CRIGR
SURFACTIN SYNTHETASE S	SULFITE REDUCTASE [NAD	INTEGRIN ALPHA-8.	SIGNAL TRANSDUCER AND	PROTO-ONCOGENE TYROSIN	PUTRESCINE-BINDING PER	VOLTAGE-DEPENDENT T-TY	D-ASPARTATE OXIDASE (E	TNF-INDUCIBLE PROTEIN	DNA POLYMERASE III, DE	NONSENSE-MEDIATED MRNA	ZEAXANTHIN EPOXIDASE P	ZEAXANTHIN EPOXIDASE P	FLAGELLAR HOOK-ASSOCIA	RIBONUCLEASE H (EC 3.1	PROBABLE MAJOR ENVELOP	LEUCOKININS PRECURSOR.	HYPOTHETICAL PROTEIN H	ZEAXANTHIN EPOXIDASE P	ARYLSULFATASE E PRECUR	HYPOTHETICAL 47.2 KD T	METHYLATED-DNAPROTEI
1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.01e+01		1.01e+01		6.80e+00	6.80e+00		6.80e+00		6.80e+00				4.54e+00	4.54e+00	4.54e+00

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Q05329;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.
EMBL;
EMBL;
PIR; P
                                                                                                                                                                                                                                                                                                                                                                                                      acid
                                    EMBL;
                                                                                                                                                                                          - PUNCTION: CATALYZES THE PRODUCTION OF GABA.
- CATALYTIC ACTIVITY: L-GLUTANATE - 4-AMINOBU-
- COFACTOR: PYRIDOXAL PHOSPHATE
- SUBUNIT: HOMODIMER (BY SIMILARITY).
- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND
                                                                                                                              the
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                          "Characterization of a linear epitope within the human pancreatic 64-kba glutamic acid decarboxylase and its autoimmune recognition sera from insulin-dependent diabetes mellitus patients."; Eur. J. Biochem. 212:597-603(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               NORTHEMANN W.
                                                                                                                                                                                                                                                                                                                                                     TISSUE-PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and primary str
                                                                                                                                                                                                                                                                                                                                                                                                                                        KARLSEN A.E., HAGOPIAN W.A., GRUBIN C.E., ADLER D.A., BARMEIER H., MATHEWES S., GRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=PANCREATIC ISLETS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD67 and GAD65) suggests that they derive from a common ancestral GAD."; Genomics 21:222-228(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU D.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         each
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BU D. F., ERLANDER M.G., HITZ B.C., TILLAKARA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAD2 OR GAD65
                                                                                                                                                                                                                                                                                                                                    WEDLINE; 93185681.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 6-585 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92196068.
                                                                                                                                                                                                                                                                                                                                                                                                                            ERNMARK A.
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                                                                                                                             European Bioinformatics Institute.
            , M81882; AAA62367.1;
, M74826; AAA58491.1;
, X69936; CAA49554.1;
, M70435; AAA52513.1;
                                                                                                                                                                                DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human glutamate decarboxylases, 65-kDa GAD and encoded by a single gene.";
. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
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                                                                                                                                                                                                                                                                                                                                                                                          Natl.
                                                                          non-profit institutions as long and this statement is not removed. s requires a license agreement (See lan email to license@isb-sib.ch).
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                                                                                                              rmatics Institute. There are no resinstitutions as long as its content
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                                                                                   (See http://www.isb-sib.ch/announce/
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Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequence analysis of a decarboxylase (GAD65).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCE2_MOUSE STANDARD; PRT; 58:
P48320; 035519;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence updi
15-JUL-1998 (Rel. 36, Last annotation updi
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM
                                                                                                                                                                                                                                                                         FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;

FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;

"Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.";

Endocrinology 133:2962-2972(1993).

-!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASADA H., KAWANTRA Y., MARUYAMA K., KUME H., DING R.G., JI F.Y., KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.; KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.; Kanbara N., KUZUME H., SANBO M., YAGI T., OBATA K.; CANBO M., YAGI T., CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C578L/6; T
MEDLINE; 97115675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6; TI
MEDLINE; 94032481.
LEE D.S., TIAN J.,
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Mus musculus (Mouse).
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Neurotransmitter biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family.

BINDING 396 396 PYRIDOXAL PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; PQ0158; PQ0158. MIM; 138275; -.
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are susceptible to seizures.",
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                                                                                                                                                between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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Pred. No. 1.14e-21;
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Neurotransmitter blosynthesis; Lysse; De Pyridoxal phosphate; Multigene family. BINDING 396 396 PYRIDOXAL E CONFLICT 259 259 F -> S (IN CONFLICT 319 319 F -> S (IN CONFLICT 325 325 K -> E (IN CONFLICT 325 325 K -> E (IN CONFLICT 499 499 P -> S (IN CONFLICT 499 P -> S (IN 
                                                                                                                                                                       EMBL; M72422; AAA63488.1; -.

PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase; D
Pyridoxal phosphate; Multigene family.
BINDING 396 PYRIDOXAL
SEQUENCE 585 AA; 65402 MW; E35D601A
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-HIPPOCAMPUS;
MEDLINE; 91299343.
ERLANDER M.G., TILLAKARATNE N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence upd
01-FEB-1996 (Rel. 33, Last annotation u
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM
(65 KD GLUTAMIC ACID DECARBOXYLASE).
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Q05683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S67454; CAB328
MGD; MGI:95634; GAD2
PROSITE; PS00392; DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two genes encode di
Neuron 7:91-100(1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOBIN A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                           146
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                                           NWELADQPQNLEEILTHCQT 165
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  NWELADOPONLEEILMHCQT
                                                                                                         Similarity
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19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396
259
319
325
6522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      distinct glutamate
                                                                                                       92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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                                                                                       Pred.
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Pred.
0; M
                                                                                                         Score 142; DB 1;
Pred. No. 1.53e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRIDOXAL PHOSPHATE (POTENTIAL).

F -> S (IN REF. 2).

I -> S (IN REF. 3).

K -> E (IN REF. 2).

P -> S (IN REF. 2).
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-> S (IN F
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                                                                                       Mismatches
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No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      decarboxylases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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1.53e-18;
                                                                                                                                                                                                                                         Decarboxylase;
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                                                                                                                                                                                           PHOSPHATE
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W REF. 3).
W REF. 2).
W REF. 2).
G CRC32;
                                                                                                                                                                           CRC32;
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                                                                                                                           Length 585;
                                                                                                                                                                                              (POTENTIAL).
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Rattus.
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DCE1_RAT
P18088;
01-NOV-1990
01-NOV-1990
01-FEB-1996
                                                                                                                                                                                BINDING
CONFLICT
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:95632; GADI.

PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase;

Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCE1_MOUSE STANDARD; PRT; 593 AA.

P48318;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

01-FEB-1996 (Rel. 33, Last annotation update)

GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)

(67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                               EMBL; Z49976; CAA90277.1; EMBL; S67453; CAB32805.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KATAROVA Z., SZABO G., MUGNAINI E "Molecular identification of the decarboxylase from the mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 198-403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                               156
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1 OR GAD67.
                                                                                                                                                                                                                                                                                                                                                                                                                          TYRDC)
                                                                                       ELSDHPESLEQILVDCR 172
                                                                                                                               similarity 52.9%;
Similarity 52.9%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94062679
                                                                                                                                                                             phosphate; Multigene family.

404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).

234 234 E -> K (IN REF. 2).

258 258 S -> T (IN REF. 1).

360 360 D -> S (IN REF. 1).

593 AA; 66584 MW; 63BC57AA CRC32;
 (Rel.
(Rel.
(Rel.
                                            STANDARD;
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33,
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2:190-202(1990).
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Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                              Score 85;
Pred. No.
                                            PRT;
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е 62
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kd form of gl
                                            593
                                                                                                                                               DB 1; Li
4.77e-05;
                                                                                                                                                                                                                                                   Decarboxylase;
                                            Å
                                                                                                                                                         Length 593;
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d other peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                     (DDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
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Matches
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JULIEN J.F., SAMAMA P
"Rat brain glutamic accona.";
                                                                                                                                                                                                                                                        EMBL; M34445; AAC42037.1; -. EMBL; X57572; CAA40800.1; -. EMBL; X57573; CAA40801.1; -. EMBL; M76177; AAA41184.1; -. PIR; A41367; A41367; PIR; A43756; A43756.
                                                                                                           CONFLICT
                                                                                                                                   CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLUTAMATE DECARBOXYLASE, (67 KD GLUTAMIC ACID DECAGAD1 OR GAD67.
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, characterization, and autoimmune recognition.";
glutamic acid decarboxylase in insulin-dependent diabetes mellitus.";
Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurognat
                                                                                                                                                                                                         PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 92020930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91014554
WYBORSKI R.J., BO
                                                                                                                                                           CONFLICT
                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MADSEN O.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICHELSEN B.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               decarboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                        156 ELSDHPESLEQILVDCR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurochem.
  w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: L-GLUTAMATE COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER.
                                                            Similarity
                                                                                               1 phosphate:

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103 10

284 28

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344 34

347 34

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                                                Conservative
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                                                           52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R. ₩.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Res.
  19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALLET J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       decarboxylase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
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                                                                                                 X
X
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                                                                                                                    L -> V (IN REF. 2).
F -> S (IN REF. 2).
EH -> AD (IN REF. 2).
AG -> EA (IN REF. 2).
T -> I (IN REF. 2).
FD -> LE (IN REF. 2).
                                              Score
Pred.
7; M
                                                                                                                                                                                            PYRIDOXAL PHOSPHATE (POTENTIAL).
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                                                                                                      -> LA (...
-> I (IN REF. 2).
) -> LE (IN REF. 2).
                                                Mismatches
                                                           86; DB 1; I
No. 4.77e-05;
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                                                                                               CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glutamic
                                                                     Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deduced from a cloned
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DDC,
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Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
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GLUTAMATE DECARBOXYLASE, 6
(67 KD GLUTAMIC ACID DECA
GAD1 OR GAD67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCE1_PIG
P48319;
01-FEB-1996
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                   099259:
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-:- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANC
-:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
  each
Proc.
[2]
                    BU D.-F., ERLANDER M.G., HITZ B.C., "IWAGNER-MCPHERSON C.B., EVANS G.A., TO WAGNER-MCPHERSON C.B. EVANS G.A."
"Two human glutamate decarboxylases,"
"Two human glutamate decarboxylases,"
each encoded by a single gene.",
Proc. Natl. Acad. Sci. U.S.A. 89:211:
                                                                                                                                                                                                                                                                   GAD1
                                                                                                                                                                                                                                                                                                                                                                                                         DCE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00392; DDC_GAD_HDC_YDC; 1. PFAM; PF00282; pyridoxal_dec; 1. Neurotransmitter biosynthesis; Lyase; Pyridoxal phosphate; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 152:257-260(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequences of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                MEDLINE; 92196068.
BU D.-F., ERLANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D31849; BAA06636.1; -
                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Cetartiodactyla;
                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                    (67 KD GLUTAMIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                           _HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphate;
                                                                                                                                                                                                      Primates;
                                                                                                                                                                                                                         Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 AA;
                                                                                                                                                             N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and expression of large isoform of decarboxylase from human pancreatic islet.", Biochem. Biophys. Res. Commun. 192:1353-1359
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDDIE MONTO
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TISSUE=PANCREATIC
MEDLINE; 93282845.
                                                                                                       This SWISS-PROT entry between the Swiss Ins
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                                                                                                                                                                                                                                                               SEQUENCE
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BU D.-F., TOBIN A.J
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EMBL/GenBank/DDBJ
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GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM
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"Glutamic acid decarboxylase cDNA: nucleotide
enzymatically active fusion protein.";
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ia; Felidae;
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4-AMINOBUTANOATE
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4 (EC 4.1.1.15)
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4.77e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata;
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Best Local
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SEQUENCE.
FAOTTO L., POLLEGIONI L.,
FAOTTO L., POLLEGIONI D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_deC; 1.

Reurotransmitter biosynthesis; Lyase; Decarboxylase;

Pyridoxal phosphate; Multigene family.

PYRIDOXAL PHOSPHATE (POTENTIAL).

BINDING 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
                                                                                                               POLLEGIONI L., CECILIANI F., CURTI B., RONCHI S., PILONE M.S., "Studies on the structural and functional aspects of Rhodotorula gracilis D-amino acid oxidase by limited trypsinolysis."; Biochem. J. 310:577-583(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
PIR;
                                                                                                                                                             CHARACTERIZATION. MEDLINE; 95382776.
                                                                                                                                                                                                Submitted
                                                                                                                                                                                                          STRAIN=CCRC
LIAW G.J., I
                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 26217;
PILONE M.S., POLLEGIONI
Submitted (APR-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                              "The primary gracilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodosporidium toruloides (Yeast) (Rhodotorula gracilis).
Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Sporidiobolaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OXDA_RHOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                 <del>:</del>
                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                      Microbiology 144:1095-1101(1998).
                                                                                                                                                                                                                                                                 "D-amino-acid oxidase gene toruloides) ATCC 26217.";
                                                                                                                                                                                                                                                                                                              STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                      ALONSO J., BARREDO
                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 ELSDHPESLEQILVDCR 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch)
                      SUBCELLULAR LOCATION: PEROXISOMAL SIMILARITY: BELONGS TO THE DAMOX/I
                                                                   CATALYTIC ACTIVITY:
NH(3) + H(2)O(2).
                                                                            FUNCTION: THIS ENZYME CAN EFFECTIVELY CONVERT CEPHALOSPORIN C INTO 7-BETA-(5-CARBOXY-5-OXOPENTANAMIDO)-CEPHALOSPORINIC ACID CATALYTIC ACTIVITY: A D-AMINO ACID + H(2)O + O(2) = A 2-OXO-AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                SUBUNIT: HOMODIMER
                                                           COFACTOR:
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A46758; A46758
   SWISS-PROT
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9; Conser
                                                                                                                                                                                                                                                                                                FROM N.A.
TCC 26217;
98240245.
                                                                                                                                                                                              CRC 20306;
., LEE Y.J.,
d (MAY-1997)
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(Rel. 32,
(Rel. 38,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  entry
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                                                                                                                                                                                                                                                                                      J.L.,
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52.9%;
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, Last annotation update)
(EC 1.4.3.3) (DAMOX) (DAO)
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                                                                                                                                                                                              E Y.H., CHEN L.L., CHU the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                           DIEZ B., SALTO F.,
ne from Rhodotorula
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Pred.
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                                                                                                                                                                                                                                                                                                                                                         MOLLA G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                       XISOMAL (POTENTIAL)
DAMOX/DASOX FAMILY
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. 4.77e-05;
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is produced through a collaboration
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databases
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                                                                                                                                                                                                                                                                                                                                                        MARTEGANI
                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodotorula
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                                                                                                                                                                                                                                                                           .L., CORTES E.; (Rhodosporidium
                                                                                2-OXO-ACID
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Matches
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                 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                            Nature 378:730-733(1995).

-!- FUNCTION: FMRFAMIDE-GATED IONOTROPIC RECEPTOR.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: MUSCLE AND MERVOUS TISSUE.
-!- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
ACT_SITE
                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. Use this requires a license agreement (See htt
                                                                                                                                                                                                             This
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                                                                                                                                                                                                                                                                                                                                                                                         Helix aspersa (Brown garden snail)
Eukaryota; Metazoa; Mollusca; Gast
Helicacea; Helicidae; Helix.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EMRFAMIDE-ACTIVATED AMILORIDE-SENSITIVE SODIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U60066; AAB51107.1; -.
EMBL; Z71657; CAA96323.1; -.
EMBL; AF003339; AAB93974.1; -.
EMBL; AF003340; AAB93975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         PFAM; PF00858; ASC; 1.
Ionic channel; Transmembrane;
                                                                                                              EMBL; X92113; CAA63084.1;
                                                                                                                                      entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         channel
                                                                                                                                                                                                                                                                                                                                MEDLINE; 96107314.
LINGUEGLIA E., CHAMPIGNY G.,
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01-NOV-1997
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PROSITE; PS00342; MICROBODIES_CTER;
      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                     FAMILY.
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                                                                                                   PS01206; ASC;
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38.9%;
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Pred. No.
7; Misma
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POLY-ASN.
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                                                                                                                                                                                                                                                                                                                     LAZDUNSKI M., BARBRY
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                                                               CYTOPLASMIC
                                                                         Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                      Gastropoda; Pulmonata; Stylommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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(See http://www.isb-sib.
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                                                               (POTENTIAL).
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15-DEC-1999
D-ASPARTATE
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CARBOHYD
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SEQUENCE
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASPARTATE AND ITS N-METHYLATED DERIVATIVE, N-METHYL D-ASPARTATE -- 1- CATALYTIC ACTIVITY: D-ASPARTATE + H(2)O + O(2) - OXALOACETATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aspartate oxidase.";
J. Biochem. 121:798-803(1997).
-i- FUNCTION: SELECTIVELY CATALYZES THE OXIDATIVE DEAMINATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SETOYAMA C., MIURA R.; Structural and functional characterization
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Homo sapiens (Human).
Tini Hominidae; Homo.
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01-NOV-1997
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OXDD_HUMAN
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241 DWNLSPDAENSREILSRC 258
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ALTERNATIVE PRODUCTS: TWO ISOFORMS; DDO-1 (SHO ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE DAMOX/DASOX FAMILY.
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COFACTOR: FAD OR 6-HYDROXYFLAVIN ADENINE DINUCLEOTIDE
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                                         Similarity 7; Conse
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01266; DAO; 1.
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9 (Rel. 39, Last anno
E OXIDASE (EC 1.4.3.1
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39, Last annotation update)
SE (EC 1.4.3.1) (DASOX) (DDO)
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58.3%;
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FAD (ADP PART) (FULL.

BY SIMILARITY.

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AICROBODY TARGETING SIGNAL (POTENTIAL).

MICROBODY TARGETING DDO-2).

MICROBOLY TARGETING SIGNAL (POTENTIAL).

MICROBOLY TARGETING SIGNAL (POTENTIAL).

MICROBOLY TARGETING SIGNAL (POTENTIAL).

MICROBOLY TARGETING SIGNAL (POTENTIAL).
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Pred. No. 2.47e-02;
5; Mismatches
                                       Score 65; DB 1; L
Pred. No. 8.57e-01;
7; Mismatches 4
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RESULT 14
ID R171_YEAST STANDARD; PRT; 183 AA. AC P05740; AC P05740; DT 01-NOV-1988 (Rel. 09, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S RIBOSOMAL PROTEIN L17-A (YL17-A).
GN RPL17A OR RPL17 OR YKL180W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC ELKaryota; Fungi; Ascomycota; Hemiascomycetes;
OC Saccharomycetaceae; Saccharomyces.
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Q00808;
15-JUL-1998
15-JUL-1998
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VEGETATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Podospora anserina encodes a protein with beta homologous domain.";
Gene 162:135-139(1995).
-:- FUNCTION: RESPONSIBLE FOR VEGETATIVE SPECIFIC INTERACTIONS WITH DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Podospora anserina.
Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
Sordariales; Sordariaceae; Podospora.
                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"A gene responsible
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(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
INCOMPATIBILITY PROTEIN HET-E-1.
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Pred. No. 8.57e-01
8; Mismatches :
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Matches
SEQUENCE FROM N.A.

RICE-FICHT A.C., CHEN K.K., DONELSON J.E.;

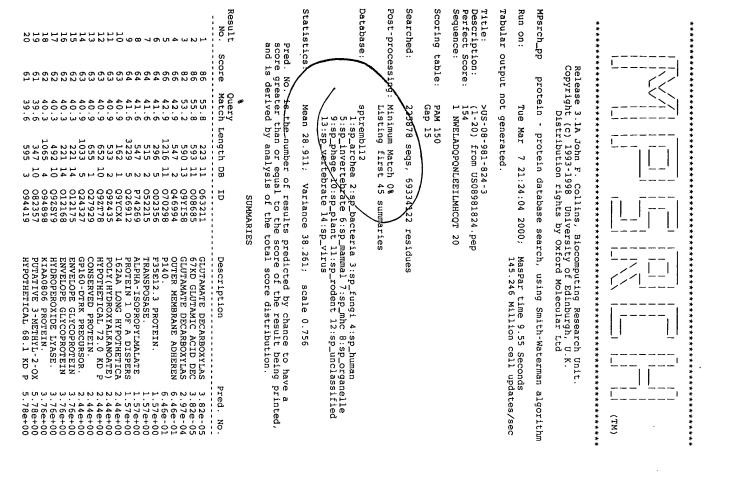
"Sequence homologies near the C-termini of the va.
glycoproteins of Trypanosoma brucei.";

nature 294:53-57(1981).

-!- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF '
TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM.
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SEQUENCE FROM N.A.
WIEMANN S., VOSS H., SCHWAGER C., RUDP T., GROTHUES D., SENSEI
STEGEMANN J., ZIMMERMANN J., ERFLE H., HEWITT N., ANSORGE W.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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EMBL; Z28179; CAA82022.1; -.
EMBL; X74151; CAA52258.1; -.
PIR; S38012; S38012.
HSSP; P48286; 1BXE.
                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 22, Last annotation update)
VARIANT SURFACE GLYCOPROTEIN ILTAT 1.3 PRECURSOR (VSG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it is supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in no was the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content is in the supported institutions as long as its content in the supported institutions as long as its content in the supported institutions as long as its content in the supported institutions as long as its
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OTAKA E., HIGO K.-I., ITOH T.;
"Yeast ribosopmal proteins: VIII. Isolation of two proteins and sequence characterization of twenty-four proteins from cytoplasmic
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei brucei
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Ribosomal protein; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIEMANN S., VOSS H., ZIMMERMANN J., GROTH
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I- MISCELLANEOUS: THERE ARE TWO GENES FOR L17 IN YEAST.
I- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS
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Similarity 43.8%;
7; Conservative
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183 AA;
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he C-termini of the variable surface
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Mismatches 6
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N C.,
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ERFLE H., HEWITT
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       THE PARASITE. THE HOST BY EXPRESSING AN ESTIMATED 1000
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SIGNAL 1 29
CHAIN 30 480
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DISULFID 42 168
DISULFID 150 206
CARBOHYD 419 419
CARBOHYD 432 432
LIPID 480 480
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                                                                                                                                                                                                                                                       PIR; S09640; S09640.
PFAM; PF00913; Trypan_glycop;
                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                 EMBL; J01221; AAA30288.1;
                                                         304 NWKPADKPANMDDYLKQ 320
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480
503 AA;
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41.2%;
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21:23:47
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BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
GPI ANCHOR.
                                                                                              Score 64; DB 1;
Pred. No. 1.31e+00
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LOW-VOLTAGE ACTIVATED	ZK783.4 PROTEIN.	KIAA0690 PROTEIN (FRAG	CHROMOSOME IV READING	PUTATIVE METHIONYL-TRN	HYPOTHETICAL 45.8 KD P	3-AMINO-5-HYDROXY BENZ	3-AMINO-5-HYDROXYBENZO	PUTATIVE PHYTOCHELATIN	HYPOTHETICAL 39.9 KD P	O KD		PROBABLE AMINO ACID OX	CONSERVED HYPOTHETICAL	HYPOTHETICAL 19.1 KD P	PR GAG-PRO-POL.	EXOGENOUS FERRIC SIDER	HERPESVIRUS 6 IMMEDIAT	R02D3.7 PROTEIN.	EG:49E4.1 PROTEIN.	UMENT PROTE	13S CONDENSIN XCAP-D2	PEG7.	KINESIN-ASSOCIATED PRO	SMAP.
1.34e+0	1.34e		1.34e+				1.34e+										8.82e+00			. 78	. 78	. 78	•	. 7

ALIGNMENTS

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RESULT
1D 008685;
AC 008685;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLREL 12, Last see
DT 01-OVL-1999 (TREMBLREL 12, Last and
DE 67KD GLUTAMIC ACID DECARBOXYLASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranid
CC Eukaryota; Metazoa; Chordathi; M
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA AUST G., STEINBRENNER H., THAMM B.,
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Best Local :
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Q63211;
01-NOV-1996
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BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;
BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;

BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;

"Developmentally regulated expression of an exon containing codon in the gene for glutamic acid decarboxylase.";

Proc. Natl. Acad. Sci. U.S.A. 87:8771-8775(1990).

EMBL; M38350; AAA41185.1; -.

PFAM; PFO0282; Pyridoxal_deC; 1.

SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia;
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3 ELADQPQNLEEILMHCQ 19
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larity 52.9%;
Conservative
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                                                       Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
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Sciurognathi; Muridae; Murinae;
                                                                                                                 Created)
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Pred. No. 3.82e-05;
7; Mismatches 1
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                             Ol-AUG-1998 (TremElrel. Ol, Created)
Ol-AUG-1998 (TremBLrel. Ol, Last sequence update)
OUTER MEMBRANE ADHERENCE PROTEIN-ASSOCIATED PROTEIN.
Escherichia coli.
Bacteria; Proteobacteria; gamma subai.
Escherichia.
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O9Y158 PRELIMINARY;

O9Y158: OTTEMBLE. 1

O1-MAY-1999 (TTEMBLE. 1

O1-NOV-1999 (TTEMBLE. 1

O1-NOV-1999 (TTEMBLE. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
-!- COFACT
-!- SIMILA
                                                                                                                                                                                                                                                                                                046994; PRELIMINARY;
046994; O1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y12257; CAA72934.1; --
PROSITE; PS00392; DDC, GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Lyase; Decarboxylase; Pyridoxal phosphate.
SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;
                                                            ZHAO S., MITCHELL S.E., MENG J., DOYLE M.P., F
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ
EMBL, U50906; AAA96312.1: -.
SEQUENCE 547 AA; 61446 MW; B737EA82 CRC32;
                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-0157:H7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of glutamate decarboxylase in chicken.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WHITE LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
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TE; PS00392; DDC_GAD_HDC_YDC; 1.
Decarboxylase; Pyridoxal phosp
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larity 52.9%;
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80B66DFF CRC32;
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No ;
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No. 2.97e-04;
DB 2;
6.46e-01
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01-JUL-1997
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070298;
01-AUG-1998
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                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAXNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSENT J., COOPER J., COOPER COPER J., COOPER J., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEWARD C. Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elsario... Caenorhabditis elegans. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditice; Peloderinae;
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                                                                                                                                                                                                                Nature 368:32-38(1994).
EMBL; Z81527; CAB04271.1;
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                                                       h 41.6%;
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1. No. 6.46e-01;
Mismatches 3;
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oderinae; Caenorhabditis.
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01-JUN-1998
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TRANSPOSASE.
                                                                                                                                                                                                                   ONA Res. 3:10 10. ONA Res. 3:1
                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
EMBL; AF038594; AAB94124.1; -
SEQUENCE 515 AA; 56566 MW; 1BAEE619 CRC32;
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052215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-PCC6803; MEDLINE; 97061201.
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Submitted (JUN-1996)
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01-FEB-1997 (TREMBLrel. 02, Las
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01-JAN-1SOPROPYLMALATE SYNTHASE.
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Bacteria; Proteobacteria; gamm
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7; Conservative
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5; Conservative
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ASUDA M.,
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Q2Z435 PRELIMINARY; PRT; 533 AA.
Q9Z435;
Q9Z435;
01-MAY-1999 (TREMBLrel. 10, Created)
01-MAY-1999 (TREMBLED 10, Last sequence update)
01-MAY-1999 (TREMBLED 10, Last annotation update)
POLY(HYDROXYALKANOATE) SYNTHASE (FRAGMENT).
PHAC2.
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   Pseudomonas
Bacteria; P
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JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., K
HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA
TAKAMIYA M., MAGUDA S., FUWAHASHI T., TANAKA T., KUDOH Y
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K.,
NOMURA N., SAKO Y., KIKUCHI H.;
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DNA Res. 6:83-101(1999).
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9 (TrEMBLrel. 12, Last annotation
HYPOTHETICAL PROTEIN.
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Pred. No. 1.57e+00;
3; Mismatches 8
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EMBL; AF042276; AAD02217.1; -.
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STRAIN=CV. COLUMBIA;
HUANG E.N., PARNELL L.D.,
DEDHIA N.N., MCCOMBIE W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                       STRAIN-DELTA H;
MEDLINE; 98037514.
                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum Archaea; Euryarchaeota; Methanobacte
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NWELADQPQNLEEILMHCQT
D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., L
DGE T., BASHIRZADEH R., BLAKELY D., COOK R.,
SON D., HOANG L., KEAGLE P., LUMM W., POTHIE
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01-JUL-1997
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024327;

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01-NOV-1996

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01-NOV-1999
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JIWANI N., CARUSO A., BUSH D., SAFER H., PAIWELL D., PRABHAKAR S.,
MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
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J. Bacteriol. 179:7135-7155(1997).
EMBL; AE000942; AAB86367.1; -.
SEQUENCE FROM N.A.
MEDLINE; 98080455.
DELWART E.L., MULLINS J.I.,
KATZENSTEIN D., WALKER B.D.,
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SIGNAL 1 23
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EMBO J. 11:391-404(1992).
EMBL; X63453; CAA45053.1; -.
HSSP; P06213; 1IRK.
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                              immunodeficiency virus type 1.
es; Retroid viruses; Retroviridae;
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Similarity 42.1%;
8; Conservative
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1033 AA;
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GP160-DTRK.
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2.55 4;
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                                                                                                                                                                                                                  "Human immunodeficiency virus type 1 populations in blood and semen.";
J. Virol. 72:617-623(1998).
EMBL; U96510; AAC40359.1; -.
PFAM; PF00516; GP120; 1.
E10velope protein.
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SEQUENCE 221 AA; 24697 MW; FDB68EB3 CRC32;
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R85598	R84337	W12405	W18865	R76657	W01797	W18846	R72271	R72272	W12404	W22305	W20064	W22306	W20065	W74717	W74716	R27221	R27222	R27220	R71733	R59516	10
	Arabidopsis thaliana a	GAD65 residues 177-191	utamic acid d	Peptide derived from h	Human 65 kD glutamine	65 kD Glutamic acid de	Glutamic acid decarbox	Glutamic acid decarbox	GAD65 residues 173-187	Rat GADII.	Rat GADII protein.		Human GADII protein.	Amino acid sequence of	equence	Full length brain GAD.	Full length islet GAD.	Brain GAD #2.	Rat glutamic acid deca	Human GAD65.	Rat GAD 65.
	1.46e+0		7.02e+00	.02€	æ	Гл			4.03e-03	2.06e-04	2.06e-0	.24€	. 24€	1.50e-07	. 506	1.50e-0	. 50	. 50	. 73	3.73e-09	

ALIGNMENTS

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Matches 2
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Albert W, Boltard C,
Albert P, Van Endert P;
708
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present peptide is a framgent of the human 65 kD glutamine decarboxylase (GAD), which can be used to diagnose, or diagnose a predisposition to, a tumour or immunological disease, preferably a autoimmune disease, especially diabetes. It can also be used as a reagent to determine specific T cell subpopulations, in medicament to treat or prevent immunological diseases, preferably autoimmune diseases, especially diabetes, to produce antigens, especially immunogens or tolerogens and to isolate specific T cell subpopulations, which can be used to produce antigens or for reinjection, optionally after inactivation.
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Human; glutamine decarboxylase; GAD; dlagnosis; predisposition; tumoun; immunological; disease; autoimmune; diabetes; reagent; determination; T cell; subpopulation; medicament; treatment; determination; production; antigen; immunogen; tolerogen; isolation; production; production; production; production; production; production; production; production; production; antigen; immunogen; tolerogen; isolation; production; productio
   W18845 standard;
W18845;
05-JAN-1998 (fi
                                                                                                                                                                                                                                                                                                                                                                                                                     subpopulations, which can be ureinjection, optionally after Sequence 20 AA;
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W01796;
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Similarity 100.0%;
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BOİtard C, Endl
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(first entry)
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Pred. No. 3.73e-09,
0; Mismatches (
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Novel cDNA encurry .....

YT Novel cDNA encurry .....

YT therapeutic and diagnostic application in insure .....

YT therapeutic and diagnostic application in insure .....

PT diabetes mellitus patients

PS Disclosure; Fig 3; 53pp; English.

CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65

CC can be used for the diagnosts and therapy of patients with autoimmune

CC diseases, esp. insulin-dependent diabetes mellitus (IDDM) and "stiff

CC man" syndrome. It is possible to use either the entire GAD65 protein

CC or polypeptide fragments of it for the immunological detection of

CC autoantibodies to GAD65 which are indicative of IDDM and other auto-

cm immune diseases. The production of this sequence by recombinant DNA

CC technology allows large scale production of eukaryotic GAD65 in its

native from without the need for separation form other proteinaceous
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23-SEP-1991; 006872.
21-SEP-1990; US-586536.
(REGC ) UNIV CALIFORNIA.
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DE19526561-A1.
DE19526561-A1.
23-\u00edra Nav-1997.
20-\u00edra Nav-1995; 026561.
20-JUL-1995; DE-026561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skin test for diagnosis of cell-mediated diseases, esp. diabetes involving intradermal admin. of auto:reactive substances claim 11; page 9; 12pp; German.

W18842-70 are peptide fragments of the 65 kD human glutamic acid decarboxylase (GAD). The fragments are autoreactive substances used for diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is determined by using a claimed method for diagnosis of cell-mediated diseases or a predisposition to cell-mediated diseases, which is effected by administering an autoreactive substance intradermally and establishing the diagnosis on the basis of the occurrence or lack of a positive reaction at the site of administration. The method is used for diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated diseases such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Donie F, Endl J, Pozzilli P, Stahl WPI: 97-088254/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 kD Glutamic acid decarboxylase peptide fragment IV. GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis; insulin-dependent diabetes mellitus; IDDM; cell-mediated disease; predisposition; autohumnune; tumour; rheumatoid arthritis;
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R23645 standard;
Sequence
                                                                                                                                                                                                                                                                          N-PSDB; Q24184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoantibodies.
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Local Similarity 100.0%;
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Pred. No. 3.73e-09;
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W09412529-A.
09-JUN-1994.
                                                                        The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acid that limit solubility. Different fragments contain epitopes for different classes of GAD65 autoantibodies.
                                                                                                                                                                                                                                               New soluble fragments of glutamic acid decarboxylase used for the diagnosis and treatment of insulin deperdiabetes mellitus and stiff man syndrome.

Disclosure: Fig. 1: 73pp; English.
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02-DEC-1993; U11705.
03-DEC-1992; US-984935
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09-NOV-1994 (fir
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Disclosure, Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD6
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03-DEC-1992; US-984935.
(REGC) UNIV CALIFORNIA.
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R59520;
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WPI; 94-200193/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stiff man syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAD65; glutamate-decarboxylase; diabetes mellitus;
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1-45 N-terminal-deleted mutant
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Similarity 100.0%;
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                    Backleskov S, Kim J, Namchuk M, Richter W, Shi Y;

WPI; 94-200193/24.

The wooluble fragments of glutamic acid decarboxylase protein -

grused for the diagnosis and treatment of insulin dependent diabetes mellitus and stiff man syndrome.

Bisclosure; Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59517) were determined. New soluble fragments of GAD65 (R59517) were determined by deletion/substitution mutagenesis. The C-terminally deleted mutants given in R59524-25 are able to recognize IDDM autoantibodies having the specificity of MICA1/MICA3. These mutants also have some N-terminal modifications or MICA2. These mutants also have some N-terminal modifications or MICA2. These mutants also have some N-terminal modifications or MICA2. These mutants also have some N-terminal modifications
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M WPI; 94-200193/24.

Y New soluble fragments of glutamic acid decarboxylase protein -

yr used for the diagnosis and treatment of insulin dependent

yr diabetes mellitus and stiff man syndrome.

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03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
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R59525;
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03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stiff man syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAD65 545-585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 TLKYAIKTGHPRYFNQLSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TLKYAIKTGHPRYFNQLSTG
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nan syndrome; autoantibody; mutagenesis.
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Similarity 100.0%;
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5 C-terminal-deleted mutant.
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Pred. No. 3.73e-09;
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D9-JUN-1993; U1705.

P 09-JUN-1993; U1705.

R 03-DEC-1992; US-984935.

R (REGC) 'UNIV CALIFORNIA.

A (REGC) 'UNIV CALIFORNIA.

PT New Soluble fragments of glutamic acid decarboxylase protein - PT New Soluble fragments of glutamic acid decarboxylase protein - PT diabetes mellitus and stiff man syndrome.

PT Used for the diagnosis and treatment of insulin dependent pt diabetes mellitus and stiff man syndrome.

PT Disclosure: Fig. 1; 73pp; English.

CC (R59517) were determined. New Soluble fragments of GAD65 (R59517) were prepared by deletion/substitution

CC (R59518-25) were prepared by deletion/substitution

CC mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for CC different classes of GAD65 autoantibodies.
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Matches 2
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Disclosure; Fig. 1; 73pp; English.

The amino acid sequences of human GAD65 (R59516) and rat GAD65 (R59519) were determined. New soluble fragments of GAD65 (R59518-25) were prepared by deletion/substitution mutagenesis. These fragments are free of N-terminal amino acids that limit solubility. Different fragments contain epitopes for
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03-DEC-1992; US-984935.
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stiff man syndrome;
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                                                                                  15-DEC-1998. 450755. 25-MAY-1995. 450755. 02-DEC-1993; US-161290. 03-DEC-1992; US-984935. 25-MAY-1995; US-450755. (REGC.) UNIV. CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; column 31-34; 30pp; English.

This sequence represents the rat glutamic acid decarboxylase protein GAD65. The invention relates to soluble fragments of a GAD65 protein that are specifically reactive with a GAD65 autoantibody (AAb), where the fragment is at least 99% pure and the AAb binds to a conformational epitope of the fragment. The soluble GAD65 fragments can be used to distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff man syndrome. They can also be used for diagnosis and treatment of IDDM and stiff man syndrome. The fragments can distinguish different temporal stages in the progression of IDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAEK/) BAEKKESKOV (KIMJ/) KIM J. (NAMC/) NAMCHUK M. (RICH/) RICHTER W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAD65; glutamic acid decarboxylase protein; rat; soluble fragment; autoantibody; insulin-dependent diabetes mellitue. Troustiff man syndrome: *horrows.
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  diabetes
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                                                                                                                                                                                                                                                                                                           GAD65;
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Solluble fragments of glutamic acid decarboxylase GAD65 - distinguish between insulin-dependent diabetes mellitus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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02-DEC-1993; US-161290.
03-DEC-1992; US-984935.
(BAEK/) BAEKKESKOV S.
                                                                                                                                                                                                                                                                           GAD65; autoantibody; solublinsulin-dependent diabetes
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PI Backkeskov S, Kim J, Namchuk M, Richter W, Shi Y;

PI Backkeskov S, Kim J, Namchuk M, Richter W, Shi Y;

DR WPI; 99-069720/06.

PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of immunoassay for GAD65 protein sequence. The invention provides tabletes and stiff man syndrome PS Examples; Fig 1; 31pp; English.

CC This represents a human GAD65 protein sequence. The invention provides coluble fragments of GAD65 that are specifically reactive with at least CC one class of GAD65 autoantibody. The fragments are substantially free of CN-terminal amino acids that would otherwise limit solibility. Different CC fragments contain different epitopes for different classes of GAD65 autoantibodies. These fragments are used in the methods of the invention CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and CC stiff man Syndrome.
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Human GAD65 protein sequence.
GAD65; autoantibody; soluble; detection; diagnosis; insulin-dependent diabetes mellitus; stiff man syndr
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This represents a human GAD65 protein sequence. The invention provides soluble fragments of GAD65 that are specifically reactive with at least one class of GAD65 autoantibody. The fragments are substantially free of N-terminal amino acids that would otherwise limit solubility. Different fragments contain different epitopes for different classes of GAD65 autoantibodies. These fragments are used in the methods of the invention for detection of GAD65 autoantibodies. The methods are used for diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and stiff man syndrome.
                                                                                                                                       Human GAD65 protein.

GAD65; glutamic acid decarboxylase protein; human; autoantibody; insulin-dependent diabetes mellitus;
                                                                               stiff man syndrome;
Homo sapiens.
                                                                                                                                                                                                                                                       W34519 standard;
W34519;
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US5849506-A.
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W86017 standard;
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25-NOV-1997
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22-FEB-1999
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  161290
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Pred. No. 3.73e-09;
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02-DEC-1993; US-161290. 03-DEC-1992; US-984935.

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                                                                                                                                                                                                                                                                            Example 1; Fig 3; 100pp; English. 086482 encode R71733 and R79105, rat and human glutamic 086481 and 086482 encode R71733 and R79105, rat and human glutamic acid decarboxylase (GAD65) respectively, from which the GAD65 fragments described in R72261-R72298 were derived. These fragments can be used to detect autoantibodies against GAD, e.g. to diagnose and treat GAD-related autolmmune disorders, such as insulin dependant diabetes mellitus or stiff man disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-1994; U09478.
17-SEP-1993; US-123859.
(REGC ) UNIV CALIFORNIA.
Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin WPI: 95-131360/17.
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(KIMJ/) KIM J.
(NAMC/) NAMCHUK M.
(RICH/) RICHTER W.
(SHIY/) SHI Y.
Baekkeskov S. Kim J. Namchuk M. Richter W.
WPI: 98-017711/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide fragments of glutamic acid decarboxylase - for diagnosis and treatment of auto:immune disease, esp. insulin dependent diabetes, also related nucleic acid, vectors, antibodies, hybridoma(s) etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1995 (first entry)
Human glutamic acid decarboxylase (GAD55).
Rat glutamic acid decarboxylase; GAD65; auotimmune disorders; insulin-dependant diabetes mellitus; stiff man disease.
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larity 100.0%;
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Pred. No. 3.73e-09;
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Pred. No. 3.73e-09;
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RESULT 15 ID W14915

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Protein; 585 AA

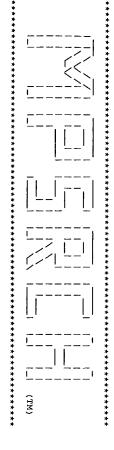
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                                                                                                                                                Claim 3; Page 13-15; 24pp; English.

A modified human glutamic acid decarboxylase (GAD) (W14915) has the native lysine residue at amino acid position 396 replaced by arginine. It is obtd. by site-directed mutagenesis (see also arginine. It is obtd. by site-directed mutagenesis (see also consisted) of native human GAD65 cDNA and expression of the mutant DNA (M5456) of native human GAD65 cDNA and expression of the mutant DNA (M5456) in transformed host cells. Lys 396 is critical for enzyme activity. By replacing it with an amino acid incapable of Schiff base formation, immunoreactivity is maintained but enzyme activity is reduced or lost, so minimising the risk of toxicity. The modified GAD can be used to treat and/or prevent autoimmune disorders such as insulin-dependent diabetes mellitus (IDDM) and other diseases, e.g. neurological diseases, esp. in individuals othering a genetic predisposition for IDDM or with an increased antibody titre against GAD.

Sequence 585 AA;
                                                                        Query Match
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Matches 2
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03-APR-1997.
27-SEP-1996; SE1210.
29-SEP-1995; SE-003379.
(SYNE-) SYNECTICS BIOTECHNOLOGY AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified glutamic acid decarboxylase for autoimmune disease treatment - has immunoreactivity of unmodified GAD65 but decreased enzyme activity, esp. useful for insulin-dependent diabetes mellitus
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WPI; 97-212895/19.
N-PSDB; T64560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified glutamic acid decarboxylase (K396R). Glutamic acid decarboxylase; GAD; autoimmune indulin-dependent diabetes mellitus; vaccine;
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10-JUL-1997 (first entry)
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:35:25 2000; MasPar time 5.65 Seconds 166.906 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Scoring table: >US-08-981-824-4 (1-20) from US08981824.pep 147 1 TLKYAIKTGHPRYFNQLSTG 20

PAM 150 Gap 15

Searched:

142080 ségs, 47172406 résidues

Post-processing: Minimum Match 0% Listing first 45 summaries

Mean-28...585; Variance 41.506; scale 0.689 1:pirl 2:pir2 3:pir3 4:pir4

Statistics:

Database:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Qy RESULT ENTRY TITLE ALTERNA ORGANIS DATE ACCESSI REFEREN #aut	#CTC #ACC #ACC #ACC #CTC #CTC #CTC ## COMMENT CLASSIF KEYWORL FEATURE FEATURE 393 SUMMARY Ouery Best Match	RESULT ENTRY TITLE ORGANIS DATE ACCESSI REFEREN #aut #tit
Db 166 TLKYAIKTGHPRYFNQLSTG 185	pession JC4064 ##molecule_type mRNA ##residues 1-585 ##label SUZ ##cross-references DDBJ_D31848; NID:g790964; PIDN:BAA06635. ##cross-references DDBJ_D31848; NID:g790965 ##cross-references DDBJ_D31848; NID:g790964; PIDN:BAA06635. ##cross-references DDBJ_D31848; NID:g790964; PIDN:g790964; PIDN:g790965 ##cross-references DDBJ_D31848; NID:g790964; PIDN:g790965 ##cross-references DDBJ_D31848; NID:g790964; PIDN:g790965 ##cross-references DDBJ_D31848; NID:g790964; PIDN:g790964; PIDN:g790965 ##cross-references DDBJ_D31848; NID:g790964; PIDN:g790964; PIDN:g790964; PIDN:g7909655 ##cross-references DDBJ_D31848; NID:g790964; PIDN:g7909655 ##cross-references DDBJ_D31848; NID:g790964; PIDN:g7909655 ##cr	RES ENT TIT ORG DAT ACC REF
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#contents annotation; intro
COMMENT This enzyme (GAD) catal
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p_position 10p11.23-10p11.23
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NCE A54778
                                                        166 TLKYAIKTGHPRYFNQLSTG 185
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##cross-references EMBL:X69936
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TLKYAIKTGHPRYFNQLSTG
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                                                                                                         100.0%;
Similarity 100.0%;
20; Conserver:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          his enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid reveral isoforms, each encoded by a separate gene. GAL also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karlsen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.; Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.; Grant, F.J.; Foster, D.; Lernmark, A. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341 Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics (1994) 21:222-228
The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterization of a linear epitope within the human pancreatic 64-kba glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.
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Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.
                                                                                                                                                                                                                     #status
#length 585 #n
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Northemann, W.
                                                                                                                                                                                                         us predicted #molecular-weight 65411 #checksum 4799
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                                                                                                                                        Score 147; DB 1;
Pred. No. 1.16e-18
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Best Local Similarity 100.0%;
Matches 20; Conservative
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#journal
#title
                                                                                                                               **PERENCE A60888

**authors Chang, Y.C.; Gottlieb, D.I.

**journal J. Neurosci. (1988) 8:2123-2130

*title Characterization of the proteins purified with

**antibodies to glutamic acid decarboxylase.

**cross-references_MUID:88258610
                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.; Tobin, A.J.

#journal Neuron (1991) 7.91-100

#title Two genes encode distinct glutamate decarboxylases

#cross-references MUID:91299343

#accession JH0423
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IFICATION #superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal RDS
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##molecule_type protein

"V',191-194,'X',196-203,'XX',206-219;'X',225-234,'X',

##residues

236-247,'X',249-266,'X';524-537,539-543,'V',547-549,
                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-585 ##label ERL
##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
                                                                                     ##status
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glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
#formal_name Rattus norvegicus #common_name Norway rat
31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L. Blochim. Blophys. Acta (1993) 1216:157-160 Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S38533
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#status predicted
#length 585 #molecular-weight 65224 #checksum 7599
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                                                                                  preliminary
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Pred. No. 1.16e-18;
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                submission
                              authors
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##cross-references GB:M38350; NID:g204231; PIDN:AAA41185.1;
#FICATION #superfamily human glutamate decarboxylase
#length 223 #molecular-weight 25069 #checksum 1
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                                                                                            ##residues
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                                                            ##experimental
                                                                       ##residues 1-585 ##label KAT
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Similarity 80.0%;
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Similarity 100.0%;
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submitted
S61533
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glutamate decarboxylase (EC 4.1.1.15) 6
glutamic acid decarboxylase
#formal_name Mus musculus #common_name
19-Mar-1997 #sequence_revision 25-Apr-1
22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775
Developmentally regulated expression of an exon containing stop codon in the gene for glutamic acid decarboxylase.
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#status predicted
#length 585 #molecular-weight 65402 #checksum 7756
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                                                                                                                                       Katarova, Z.; Szabo, G.;
Eur. J. Neurosci. (1990)
Molecular identification
decarboxylase from the
                                                                                                                                                                                                    $61534; $61533
$61534
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                              Szabo,
                                             861533
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Pred. No. 1.16e-18;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134; DB 2;
Pred. No. 1.62e-15;
              EMBL
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             Data
                                                                                                                                        of the mouse.
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2:190-202
             Library,
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25-Apr-1997 #text cl
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02-Jul-1996 #text_change
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
#journal
                                                                                                                                                                                                                                                             #authors Julien, J.F.; Samama, P.; Mallet, J.
#journal J. Neurochem. (1990) 54:703-705
#title Rat brain glutamic acid decarboxylase
#title cloned cDNA.
#cross-references MJID:90132703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title Characterization of decarboxylase. #cross-references_MUID:91014554
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                  ##molecule_type mRNA
1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',
##residues
348-351,'LE',354-379,'R',381-593 ##label JUL
##cross-references GB:X57572; NID:956185; PINN:CAA40800.1; PID:956186
NT This enzyme (GAD) catalyzes the formation of an inhibitory
rhis enzyme (GAD) catalyzes the formation of an inhibitory
gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
it has several isoforms, each encoded by a separate gene.
IFICATION #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
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1-554,'YQPQGDKANFFRMVISNPAASQSDIDFLTEEIERLGQDL'
                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-593 ##label WYB
##cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184
##note the authors translated the codon TGT for residue 412;
Ser and TCT for residue 413 as Cys
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##residnon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I. Brain Res. Mol. Brain Res. (1990) 8:193-198 Characterization of a cDNA coding for rat g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A. Dyrberg, T.; Madsen, O.D.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
Cloning, characterization, and autoimmune recognition islet glutamic acid decarboxylase in insulin-depende diabetes mellitus.
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glutamate decarboxylase (EC 4.1.1.15) 1 - rat
glutamate decarboxylase (AD67; L-glutamate 1-carboxy-lya
#formal_name Rattus norvegicus #common_name Norway rat
12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
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Pred. No. 1.62e-15;
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Best Local Similarity 80.0%;
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##cross-references EMBL:222750

#ICATION #superfamily human glutamate decarboxylase

Carbon-carbon lyase; carboxy-lyase

#Iength 593 #molecular-weight 66952 #checksum
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                                   174 TLKYGVRTGHPRFFNQLSTG 193
                                                                                                                                                                                                                                                         ##status preliminary
##molecule_type mRNA
##residues 1-593 ##label JOH
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S51775
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#formal_name Homo sapiens #common_name man
15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
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Nucleotide sequence and chromosomal assignment of a cDNA
                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, May 1993 \$51776
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#formal_name Homo sapiens #common_name man
14-111-1995 #sequence_revision 10-Nov-1995 #text_change
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    #status predicted
jth 593    #molecular-weight 66640    #checksum 3971
                                                                                                                                                                                                                   this is an unpublished revision to the sequence
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                                                                                          91.2%;
80.0%;
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Pred. No. 1.62e-15;
                                                                                          Score 134; DB 2;
Pred. No. 1.62e-15;
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Pred. No. 1.62e-15;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Yamashita, K.; Cram, D.S.; Harrison, L.C.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title Molecular cloning of full-length glutamic acid decarboxylase
for from human pancreas and islets.
#cross-references_MUID:93282844
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##molecule_type mRNA
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#accession B41935
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#accession PQ0157
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                            ##experimental
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##residues______218-463__##label_CR1
                                                                               ##residues
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##experimental_source pancreatic islet
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##cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936
##experimental_source pancreatic islet
##anote sequence extracted from NCBI backbone (NCBIP:88006)
                                                        ##cross-references GB:M70434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##experimental_source pancreatic islet
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PQ0158
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Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;
Akazawa, S.; Miyamoto, T.; Nagataki, S.
Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
Cloning and expression of large isoform of glutamic acid
decarboxylasse from human pancreatic islet.
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                                                                                                                                                                          Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
Cloning and partial nucleotide sequence of human glutamic
acid decarboxylase cDNA from brain and pancreatic islets.
                                                                                                                                                                                                                                                  Cram, D.S.; Barnett, L.D.; Joseph,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, Lancet (1991) 338:1468-1469
Cloning of large isoform of human brain glutamic
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Two human glutamate decarboxylases, 65-kDa GAD and
GAD, are each encoded by a single gene.
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B.; Evans, G.A.; Tobin
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##molecule_type mRNA
218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,
"D',331-338,'L',340-390,'S',392-397 ##label CR2
##cross-references GB:M70435; NID:g182941; PIDN:AAA52513.1; PID:g182942
##experimental_source pancreatic islet
                                           ACCESSIONS
REFERENCE
#authors
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405
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COMMENT This enzyme (GAD) catalyses the formation of an inhibitory
neurotransmitter gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
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ENTRY
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CLASSIFICATION #superfa
KEYWORDS alternat
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Best Local Similarity 80.0%;
Wutches 16; Conservative
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#accession B41367
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                                                                                                      JC4065 #type complete
glutamate decarboxylase (EC 4.1.1.15) 67K chain - pig
#formal_name Sus scrofa domestica #common_name domestic
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *superfamily human glutamate decarboxylase alternative splicing; carbon-carbon lyase; phosphoprotein; pyridoxal phosphate
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S.; Skog, S.; Hoekfelt, T.; Ritzen, E.M.
Mol. Cell. Biol. (1990) 10:4701-4711
Expression of the neurotransmitter-synthesizing of
gluttamic acid decarboxylase in male germ cells
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Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758

Cloning, characterization, and autoimmune recognition of islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
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The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestra
                      Suzuki, R.; Asami, N.; Asami (1995) 152:257-260
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COMMENT This enzyme catalyzes the conversion of glutamic acid
gamma-amino butyric acid.

CLASSIFICATION #superfamily human glutamate decarboxylase
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Best Local Similarity 80.0%;
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#cross-references_MUID:95137399
                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 TLKYGVRTGHPRFFNQLSTG 194
                                                ##residues 1-594 ##label KOB
##cross-references GB:M18629; NID
                                                                                                                                                                                                                                                                                                                                                                   175 TLKYGVRTGHPRFFNQLSTG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
##residues 1-594 ##label JOH
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PID:d1007208; PID:g790967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references EMBL:222750; NID:g298098; PIDN:CAA80435.1;
PID:g298099
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                                                                              ##molecule_type mRNA
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Similarity 80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnstone, A. submitted to S51775
                                                                                                                                                                             glutamate decarboxylase (EC 4.1.1.15) 1 - cat
glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
#formal_name Felis silvestris catus #common_name domestic
31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase
Kobayashi, Y.;
J. Neurosci. (1
                                                                                                                  submitted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $$1775 #type complete
glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo saptens #common_name man
15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain DOPA decarboxylase binding #status
#label BIN
#length 594 #molecular-weight 66894 #checksum
                                  A45671
                                                                                                  A46758
                                                                                                                                Kobayashi,
                                                                                                                                                   A46758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary
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                                                                                                                                                                                                                                                                  #type complete
 .; Kaufman, D.L.; T
(1987) 7:2768-2772
                                                                                                                  GenBank,
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                                                                                                                                  Kaufman,
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Pred. No. 1.62e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 134; DB 2;
Pred. No. 1.62e-15;
                                                NID:g163858; PIDN:AAA51430.1;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                               September
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                                                                                                                  Tobin,
er 1989
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ACCESSIONS
REFERENCE
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CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE
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                                                                                                                                                       SUMMARY
                                                                                                                                                                                                            FEATURE
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                                                                          Matches
                                                                                          Query Match
Best Local Similarity
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Best Local Similarity 80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                   #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:90155291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #accession
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                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-510 ##label JAC ##cross-references GB:X76198; NID:g433082; PIDN:CAA53791.1; PID:g433083
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                                     92
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                     TLKYQVKTGHPHFFNQLSNG 111
TLKYAIKTGHPRYFNQLSTG
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this sequence has been revised in reference A46758
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each enroded by a constant
                                                                                                                                                                                                                                                                                                                                      idues 156-200,'F',202-300,'K',302-384,'L',386-510 ##label JA2
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid,
it has several isoforms, each encoded by a separate gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jackson, F.R.; Newby, L.M.; Kulkarni, S
J. Neurochem. (1990) 54:1068-1078
Drosophila GABAergic systems; sequence
glutamic acid decarboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Drosophila melanogaster)
L-glutamate 1-carboxy-lyase
#formal_name Drosophila melanogaster
25-Oct-1989 #sequence_revision 23-Mar-1995
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JH0192
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                                                                                                                                                   #length
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                                                                                                                                                 #status predicted
1510 #molecular-weight 57758
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                                                                                          83.7%;
75.0%;
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Pred. No. 1.62e-15;
                                                                                          Score 123; DB 1;
Pred. No. 6.52e-13
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                                                                                                          Length 510
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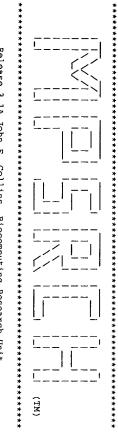
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ACCESSIONS
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CLASSIFICATION
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                                                                                   Query Match
Best Local
                                                                    Matches
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Reymond, I.; Sergeant, A.; Tappaz, M.
#journal Biochim. Biophys. Acta (1996) 1307:152-156
#title Molecular cloning and sequence analysis of the cDNA encoding
rat liver cysteine sulfinate decarboxylase (CSD).
#cross-references MUID:96283809
#accession $71489
                                                                                                                                                                                                                                                                                  #contents
                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #accession
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the author's name has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
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                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-177,'V',179-457,'M',459,'PGPTSSEWWWPTPYWSRPI' ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##experimental_source liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:X94152;
PID:e218415;
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##residues 1-493 ##label REY
                                                                                                                                                                                                                                                                                                                                                        ##residues
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                               78 IHYSVKTGHPRFFNQLFSG 96
2 LKYAIKTGHPRYFNQLSTG
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                                                                                     n 73.5%;
Similarity 63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $71489 #type complete sulfoalanine decarboxylase (EC 4.1.1.29) cysteine sulfinate decarboxylase; cysteine decarboxylase
                                                                                                                                                                                                                                             annotation; erratum this a correction of the author's name from *superfamily human glutamate decarboxylase
                                                                                                                                                                                                                                                                                                 Kaisaki, P.J.; Jerkins, A.A.; Goodspeed, Biochim. Biophys. Acta (1995) 1263:179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S55689
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$71489
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09-Dec-1997 #sequence_revision
                                                                                                                                                                                                                              carbon-carbon
                                                                                                                                                                                                                                                                                                                                          S60723
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                                                                                                                                         #length 493
                                                                    Conservative
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                                                                                                                                                                                                               phosphate
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                                                                                                                                                                                                                                                                                                                                                        220-230 ##label KA2
                                                                                                                                                                                                                                                                                                                                                                                        preliminary
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                                                                                                                                                           #status
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:M64755;
PID:g847653
                                                                                                                                       #molecular-weight 55248
 20
                                                                                                                                                                                                                              Iyase; carboxy-lyase; phosphoprotein; pyridoxal
                                                                Score 108; Db 2,
Pred. No. 1.83e-09;
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PID:g1263164
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09-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN: AAC42063.1;
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                                                                                                     Length 493;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

1110 CITE Tue Mar 7 21:30:29 2000; MasPar time 3.48 Seconds 171.790 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-981-824-4 (1-20) from US08981824.pep 147 1 TLKYAIKTGHPRYFNOLSTG 20

Searched: Scoring table: PAM 150 Gap 15

Post-processing: Minimum Match 0% Listing first 45 summari 82229 seqs, 29864866 res

Mean 29.209; Variance 38.246; swiss-prot38 1:swissprot

scale 0.764

Statistic

Database:

Pred No. is the-number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222223	Result No.
11447 11447 113447 113447 113447 113447 113447 113447 113447 113447 1134	Score
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163786 18394 18394 18394 18394 18394 18394 18394 18394 18394 18394	Length
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ALIGNMENTS

DCD2_RAT CRED-1996 (Rel. 33, Careated) D1-FEB-1996 (Rel. 33, Last sequence update) D1-FEB-1996 (Rel. 33, Last sequence update) D1-FEB-1996 (Rel. 33, Last annotation update) GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1. (65 KD GLUTAMIC ACID DECARBOXYLASE). GAD2 OR GAD65. Rattus norvegicus (Rat). ERLAND2 GRAD65. RATUS OR GAD65. RATUS OR GAD64. RATUS OR GA	AA. je) late) sc 4.: c y mus. m S. mrbox:	1.1.1 brata rinae rinae
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative EMBL; M7422; AAA63488.1; -.

PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase; Decarboxylase;

Pyridoxal phosphate; Multigene family.

Pyridoxal phosphate; Multigene family. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Score 147; DB 1; Pred. No. 6.54e-21; 0; Mismatches 0 Length 585;

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DCE2_PIG
P48321;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15)
(65 KD GLUTAMIC ACID DECARBOXYLASE).
 MEDLINE; 9
                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
BINDING. 396
PYRIDOXAL PHOSPHATE (POTENTIAL).
SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15)
(65 KD GLUTAMIC ACID DECARBOXYLASE).
                                                    Eutheria;
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01-FEB-1996
                                                                                                                                                                                     DCE2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Local Similarity 100.0%;
nes 20; Conservation
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FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2)

COFACTOR: PYRIDOXAL PHOSPHATE.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, I
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                                                                sapiens (Human)
ryota; Metazoa;
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64-kDa glutamic acid decarboxylase and its autoimmune recognition sera from insulin-dependent diabetes mellitus patients."; Eur. J. Biochem. 212:597-603(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ecid decarboxylase Proc. Natl. Acad. S
                                                                                                                 PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; Pyridoxal_dec; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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EMBL; M74826; AAA58491.1;
EMBL; X69936; CAA49554.1;
EMBL; M70435; AAA52513.1;
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                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTE
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD67 and GAD65) suggests that they derive from a common ancestral GAD."; Genomics 21:222-228(1994).
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WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;
"Two human glutamate decarboxylasss, 65-kDa GAD
each encoded by a single gene.";
Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992)
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                                                      Local Similarity hes 20; Conser
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U.S.A. 88:8337-8341(1991).
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                                                    Mismatches
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Endocrinology 133:2962-2972(1993).
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-i- CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).
-i- COPACTOR: PYRIDOXAL PHOSPHATE.
-i- COPACTOR: PYRIDOXAL PHOSPHATE.
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LEE D.S., TIAN J., PHAN T., KAUFMAN "Cloning and sequence analysis of a decarboxylase (GAD65)."; Biochim. Blophys. Acta 1216:157-160(
                                                                                                                                                                                                                                          EMBL; L16980; AAA93049.1; -.
EMBL; D42051; BAA22893.1; -.
EMBL; S674549; CBAB22803.1; -.
MGD; MGI:95634; GAD2
PROSITE; PS00392; DCC_GAD_HDC_YDC;
PROSITE; PS00392; DCC_GAD_HDC_YDC;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
65 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                    PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; L
Pyridoxal phosphate; Multigene f
                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASADA H., KAWAMURA Y., MARUYAMA K., KUME H., DING R.G., JI F.Y., KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.; "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase (GAD65) maintain normal levels of GAD67 and GABA in their brains are susceptible to seizures.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6; T:
MEDLINE; 97115675
                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94062679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 175-379 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                         166 TLKYAIKTGHPRYFNQLSTG
سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: LOCAL TO DOPA DECARBOXYLASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DECARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR GAD65.
TLKYAIKTGHPRYFNQLSTG
                                                         Similarity
20; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia;
                                                      100.0%;
larity 100.0%;
Conservative
                                                                                                    259
319
325
499
65224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                     synthesis; Lyase; Decarboxylase;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1216:157-160(1993).
                                                                                                                   MW.
20
                            185
                                                                    Score
Pred.
                                                                                                             PYRIDOXAL PHOSPHATE (POTENTIAL).

F -> S (IN REF. 2).

I -> S (IN REF. 3).

K -> E (IN REF. 2).

P -> S (IN REF. 2).

; 9BE5C088 CRC32;
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                                                                      147; DB 1;
No. 6.54e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         murine
                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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                                                                                                                                                                                                                                                                                                                                                                  Usage
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                                                                                   Length 585
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RESULT

ID DCEL_MOUSE STANDARD; PRT; 593 AA. AC P48318;

DT 01-FEB-1996 (Rel. 33, Careated)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1)

GN 061D1 OR GAD67.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Verteb

CC Eutheria; Rodentia; Sciurognathi; Muridae; Mur

RN (1)

RT SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

EUR. J. Neurosci. 2:190-202(1990).

RI 2010ENCE OF 198-403 FROM N.A.

RT SEQUENCE OF 198-403 FROM N.A.

RT SULLKNER-JONES B.E., CRAM D.S., KUN J., HARRIS

RT LOCALIZATION and quantitation of expression of decarboxylase genes in pancreatic beta-cells ar

rissue-brain;

RT LOCALIZATION AND S.A.

RT LOCALIZATION AND S.A.

RT LOCALIZATION AND S.A.

RT LOCALIZATION CATALYZES THE PRODUCTION OF GABA

CC -:- SUBUNIT HOMODIMER (BY SIMILARITY).

CC -:- SUBUNIT HOMODIMER (BY SIMILARITY).

CC -:- SUBUNIT HOMODIMER (BY SIMILARITY).

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CC the European Bioinformatics Institute. There

CC use by non-profit institutions as long as

CC modified and this statement is not removed. U

CC entities requires a license@isb-sib.ch).

DR MGDJ, MGI:9532; GAD1.

DR MGDJ, MGI:9532; GAD1.

PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PROSITE: S933, AA; 66584 MW; 63BC57AA CRC32;

SQ SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;
RESULT
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Best Local S
Matches 1
DCE1_RAT
P18088;
01-NOV-1990
01-NOV-1990
01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.; "Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other periph
                                                                                                                                                                 174 TLKYGVRTGHPRFFNQLSTG
||||:::||||::||||||
1 TLKYAIKTGHPRYFNQLSTG
                                                                                                        σ
                                                                                                                                                                                                                                                    Similarity 80.0% 16; Conservative
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0282; pyridoxal_dec; l.

psnitter blosynthesis; Lyase; Decarboxylase;

L phosphate; Multigene family.

L phosphate; Multigene family.

PYRIDOXAL PHOSPHATE (POTENTIAL).

24 404

24 E -> K (IN REF. 2).

258 258 S -> T (IN REF. 1).

258 258 C -> S (IN REF. 1).

260 360 D -> S (IN REF. 1).
(Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 33, Last annotation updat
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                        91.2%;
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                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                      Score 134;
Pred. No. 1.
                                                                                   PRT;
                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               moved. Usage by and for (See http://www.isb-sib.
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4-AMINOBUTANOATE
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..91e-17;
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ae; Murinae;
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as its content
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of glutamic
                                                                                                                                                                                                                                                                                            Length 593;
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Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
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MBL outstation -
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Best Local
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, characterization, and aurosmmune recognization glutamic acid decarboxylase in insulin-dependent diabetes mellitus.";
Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAD1
                                                                                                                                                                                                 PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase; Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                                                        EMBL; M34445; AAC42037.1; -. EMBL; X57572; CAA40800.1; -. EMBL; X57573; CAA40801.1; -. EMBL; M76177; AAA41184.1; -.
                                                                                           SEQUENCE
                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                  PIR; A41367; A41367
PIR; A43756; A43756.
                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: L-GLUTAMATE = -!- COFACTOR: PYRIDOXAL PHOSPHATE. -!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JULIEN J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     decarboxylase.";
Brain Res. Mol. Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WYBORSKI R.J., BOND R.W
"Characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67) (67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MADSEN O.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MICHELSEN B.K., PETERSEN J.S., BOEL E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
           174 TLKYGVRTGHPRFFNQLSTG
د.
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1 OR GAD67.
                                                                                                                                                                                                                                                                                                                                                                                  European
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                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the ED
European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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brain glutamic aci
                                                         Similarity
                                             16;
                                                                                                                                                                                                                                    PS00392; DDC_GAD_HDC_YDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92020930
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Rodentia;
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103
284
287
344
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380
                                            Conservative
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103
                                                       91.2%;
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                                                                                           66640 MW;
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                     193
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                                                                                                    EH -> AD (IN REF. 2).
AG -> EA (IN REF. 2).
T -> I (IN REF. 2).
FD -> LE (IN REF. 2).
L -> R (IN REF. 2).
                                                         Pred.
                                                                   Score
                                            4.
                                                                                                                                                                L -> V (IN REF. 2).
F -> S (IN REF. 2).
                                                                                                                                                                                      PYRIDOXAL PHOSPHATE (POTENTIAL).
                                                                                           5A0B67C0
                                            Mismatches
                                                       134; DB 1;
No. 1.91e-17;
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for rat
                                                                                                                                                                                                               Decarboxylase;
                                                                                           CRC32;
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                                            0;
                                                                 Length 593;
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                                            Indels
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Rattus.
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MBL outstation -
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RESULT

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P48319;
01-FEB-1996
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                Q99259;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence upd
01-QCT-1996 (Rel. 34, Last annotation u
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM
(67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANC
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
TYRDC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euxaryota; Cetartiodactyla; Suina; Suidae; Sus.
  Proc.
                                                                                                                                                                                                                                                                                                                                                                                                         DCE1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_dec; 1.
Neurotransmitter biosynthesis; Lyase;
Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                  WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN
"Two human glutamate decarboxylases, 65-k
each encoded by a single gene.",
exoc. Natl. Acad. Sci. U.S.A. 89:2115-211
                                                                                                MEDLINE; 92196068.
BU D.-F., ERLANDER M.G.,
                                                                                                                                                                                                                                                               GAD1 OR GAD.
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"Sequences of two
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                                                                                                                                                                                                       Eutheria; Primates;
                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                             SEQUENCE FROM N.A
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39, Control of the                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             porcine
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                                                                                                  B.C.,
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                    89:2115-2119(1992)
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No. 1.
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L.91e-17;
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
MEDLINE;
BU D.-F.,
                                                                                                                                                                                                           "Expression of the neurotransmitter-synthesizing decarboxylase in male germ cells."; Mol. Cell. Biol. 10:4701-4711(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE: 93282844.
YAMASHITA K., CRAM D.S., HARRISON
"Molecular cloning of full-length
human pancreas and islets.";
Biochem
                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                           This
                                                                                                                                                                                                                                                                                                       CRAM D.S., BARNETT L.D. "Cloning and partial nu decarboxylase cDNA from Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE-PANCREATIC MEDLINE; 93282845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELLY C.D., EDWARDS Y., JOHNSTONE A.P MUSSEY S.S., POVEY S., CARTER N.D.; "Nucleotide sequence and chromosomal the large isoform of human glutamate Ann. Hum. Genet. 56:255-265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The exon intron organization of the two human glutamate decarboxylases (G they derive from a common ancestral C
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PERSSON H.,
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SEQUENCE OF 527-594
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                                                                                                      ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                         SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS
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 M81883;
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                                                             equires a license agreement (Semail to license@isb-sib.ch).
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AAA62368.1;
AAB59427.1;
CAA80435.1;
AAB26937.1;
AAB26938.1;
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., MIYAMOTO T.;
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EMBL; M55574; AAA72938.1
EMBL; A28074; CAA01913.1
PIR; PQ0157; PQ0157.
MIM; 266100; -.
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between the Swiss Institute of Bioinformatics and the EMBL on the European Bioinformatics Institute. There are no restrictic use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.cl
                                                                                                            GAD1
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01-OCT-1993 (Rel. 27, Last sequence up
01-FEB-1996 (Rel. 33, Last annotation
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORE
(67 KD GLUTAMIC ACID DECARBOXYLASE).
                                                                                                                                                                                                                                   TISSUE=OCCIPITAL CORTEX; MEDLINE; 87310623.
                                                                                                                                                                                                                                                                                                     Felis silvestris
Eukaryota; Metaz
                                                      This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                        "Glutamic acid decarboxylase
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Eutheria;
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D5 PYRIDOXAL PHOSPHATE (POTENTIAL).
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PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_deC; 1.

Neurotransmitter biosynthesis; Lyase;

Pyridoxal phosphate.

Pyridoxal phosphate.

BINDING 322 322 PYRIDOXAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P20228:
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
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PIR; A45758; A46758.

PIR; A46758; A46758.

PROSSITE; PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase; Decarboxylase;

Pyridoxal phosphate; Multigene family.

PYRIDOXAL PHOSPHATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                             EMBL; X76198; CAA53791.1; -. PIR; A30999; A30999. PIR; JH0192; JH0192.
                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAD
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Neurochem. 54:1068-1078(1990).
J. Neurochem. 54:1068-1078(1990).
J. FUNCTION: CATALYZES THE PRODUCTION
J. CATALYTIC ACTIVITY: L-GLUTAMATE = 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JACKSON F.R., NEWBY L.M., KULKARNI "Drosophila GABAergic systems: sequation decarboxylase":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation . Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: PYRIDOXAL SUBUNIT: HOMODIMER.
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                                                                                                                                                                               510 AA;
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Drosophilidae; Drosophila.
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4-AMINOBUTANOATE
                                                                                                                                                                                                                                             Decarboxylase;
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                                                                                                                                                                             PHOSPHATE (POTENTIAL).
1 CRC32;
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There are no restrictions
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1.91e-17;
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01-JUL-1993 (Rel. 2
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DIHYDROOROTASE (EC
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
HYPOTHETICAL 46.9 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGIQ_ECOLI
Q46861;
                                                                                                                                   "The Ustilago maydis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT
                                                                   -!- CATALYTIC
                                                                                        analysis.";
Gene 117:73-79(1992)
                                                                                                                                                                                                                                                                                                  Ustilago maydis (Smut fungus).
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
                                                                                                                                                                                                                                                                                                                                                    PYR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 413 AA; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U28377; AAA69183.1; -. EMBL; AE000383; AAC76051.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
SIMILARITY: TO THE C-TERWINAL OF M.JANNASCHII MJ1155. THE TERWINAL PART OF MJ1555 IS COLINEAR TO E.COLI YGIR. ALSO SIMILARITY TO FAMILY UPF0004.
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PATHWAY: THIRD STEP
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C 3.5.2.3) (DHOASE).
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KD PROTEIN IN METC-SUFI INTERGENIC REGION
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                                                                   DIHYDROOROTATE
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PYRIMIDINE BIOSYNTHESIS
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Pred. No. 6.51e-02;
6; Mismatches 5
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ACOC_CUCMC STAND....

Q42569;

I 01-NOV-1997 (Rel. 35, Created)

I 01-NOV-1997 (Rel. 35, Last sequence update)

I 01-NOV-1997 (Rel. 35, Last annotation update)

CONTRASE (EC 4.2.1.3) (ACONITATE HYDRATASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
Matches
                                                                                                                                                                                                                                        SEQUENCESTRAIN=CV. CAN.
STRAIN=CV. CAN.
95229629.
PROFITE PEREZ F
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; euphyllophytes; Spermatoph core eudicots: Porta
                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                            with mammalian iron responsive element-binding with mammalian iron responsive element-binding J. Biol. Chem. 270:8131-8137(195).

-i- CATALYTIC ACTIVITY: CITRATE - CIS-ACONITATE - CATALYTIC ACTIVITY: CITRATE - CIS-ACONITATE - CATALYTIC GLYOXYLATE BYPASS, PLAYS A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
SEQUENCE
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modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
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METAL
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                                                                 ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                          SIMILARITY: BELONGS
                                                                                                                            MISCELLANEOUS: ACONITASE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE (3FE-4S) FORMS. THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE THAT INTERCONVERTS CITRATE, CIS-ACONITASE, AND
                                                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC MISCELLANEOUS: ACONITASE HAS AN AC
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JQ1667;
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X82840;
P20004;
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PS00483; DIHYDROOROTASE_2;
ne blosynthesis; Hydrolase;
ne 5 15 2INC (F
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JQ1667.
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Rosidae; eurosids
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                                                                                                          TO THE ACONITASE/IPM ISOMERASE FAMILY.
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Streptophyta; Embryophyta; Tracheophyt
hyta; Magnollophyta; eudicotyledons;
urosids I; Cucurbitales; Cucurbitaceae;
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INC (POTENTIAL).
6E60A4C9 CRC32;
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LAYS A ROLE IN
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                                              ormatics and the EMBL outstation
There are no restrictions on it
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yed. Usage by and for commercia
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GLUCONEOGENESIS
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Query Match
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METAL 372

METAL 375
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01-NOV-1997
   Lyase; Gl
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SEQUENCE
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                                                                                               EMBL; X82839; CAA58046.1; ALT_INIT. HSSP; P16276; 6ACN.
PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
PFAM; PF00330; aconitase; 1.
                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PEYRET P., PEREZ P., ALRIC M.;
"Structure, genomic organization, and expression thaliana aconitase gene. Plant aconitase show si with mammalian iron-responsive element-binding p J. Biol. Chem. 270:8131-8137(1995).

-i- CATALYTIC ACTIVITY. CUTTRATE—CIS-ACONITATE
-i- PATHWAY: GLYOXYLATE BYPASS, PLAYS A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Stretta; Embryophyta; Tracheophy
Eukaryota; Viridiplantae; Stretta; Embryophyta; Tracheophy
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                              PFAM; PF00330; aconitase; 1. PFAM; PF00694; Aconitase_C;
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PFAM; PF00694; Aconitase_C;
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                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way.
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                                                                                                                                                                                                                                                                                                                        ISOCITRATE. SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          STORED OIL. SUBCELLULAR LOCATION: CYTOPLASMIC
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PS01244;
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897 i
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ACONITASE_2;
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                                                                   Iron-sulfur;
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ron-sulfur; 4Fe-4S,
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
W; FB556DFE CRC32;
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4.02e-01
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Best Local Similarity 46.2%;
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                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOMESTATY, B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FIT2HUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., MGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).

-i- FUNCTION: COULD BE INVOLVED IN CELL WALL DEGRADATION OR FORMATION (BY SIMILARITY).

-i- SIMILARITY: STRONG, TO E.COLI YEBA.

-i- SIMILARITY: TO STAPHYLOCOCCUS LYSOSTAPHIN.
                                                                                                                                                                                                               TIGR; HI0409; -.
PFAM; PF001551; Peptidase_M37; 1.
Hypothetical protein; Cell wall.
SEQUENCE 475 AA; 53255 MW; 80
                                                                                                                                                                                                                                                                                     EMBL; U32724; AAC22068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RD / KW20;
MEDLINE; 95350630.
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                                                                     4 YAIKTGHPRYFNO 16
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(Rel. 32, Last sequence update)
(Rel. 32, Last snnotation update)
L PROTEIN HI0409.
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PRT; 0, Created) 0, Last sec 2, Last ann 7. ata; Crania Phasianidae	4; Mism 193 20	GOTTLIEB D. d expression tamic acid d S.A. 87:8771 deC: 1. MW; C7162A Fred. No.	PRT; 1, Created) 1, Last sequ 8, Last anno 8, Craniat ognathi; Muz		093327 093327 093327 093327 053154 045311 P87134 P87134 049561 020561 020561 020857 049665 049665 073117 022080 09714665 022080 09714663 09714663 09714663 09714663 09714663 09714663 09714663 09714663 09714663 09714663 09714663
590 AA. ence update) tation update) s; Vertebrata; Archosauri Phasianinae; Gallus.	atches	I.; of an exon containing a ecarboxylase.*; -8775(1990). C1 CRC32; ; DB 11; Length 223; 6.34e-18; Table	223 AA. lence update) ptation update) a; Vertebrata: Mammalia; idae; Murinae: Rattus.		HISTONE MACKOHZALI. HISTONE MACROHZALI. HISTON
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ACCOMMENDATION
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01-JUL-1997 (TrEMBLrel. 04, Last sequence
01-NOV-1999 (TrEMBLrel. 12, Last annotatio
67KD GLUTAMIC ACID DECARBOXYLASE
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y12257; CAA72934.1; --
PROSITE; PS00392; DDC_GAD_HDC_YDC;
PFAM; PF00282; pyridoxal_deC; 1.
Lyase; Decarboxylase; Pyridoxal pho
SEQUENCE 593 AA; 66648 MW; BAFI
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                                                          ZENG L.-W., COMERON J.M.,
Genetica 0:0-0(1997).
EMBL; AF025807; AAB87892.1
HSSP; P06543; 1QOD.
                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                 Ephydroidea;
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AUST G., STEIN
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)
-i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAGBERG
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                                  YBASE;
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SE; FBgn0023295; 
PF00282; pyridox
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16; Conse
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larity 80.0%;
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023295; Dpse\Gad1 pyridoxal_deC; 2
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66710 MW;
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BAFE92E0 CRC32;
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No. 6.34e-18;
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. 6.34e-18;
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044103;
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01-JUN-1998
01-JUN-1998
01-NOV-1999
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Genetica 0:0-0(1997).
GENBL; AF025808; AAB87893.1
HSSP; P06543; 1QOC.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAD1
                                                                                                                              PRITCHARD J.E., RAMSDEN D.B.;
"Human cysteine sulfinic acid decarboxylase (Carbonitted (DEC-1998) to the EMBL/GenBank/DDBJ EMBL; AF116545; AAD32543.1; -.
                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominid
                                                                                                               SEQUENCE
                                                                                                                                                                                                   TISSUE-BRAIN;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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1998 (TrEMBLrel. 06, I
1999 (TrEMBLrel. 12, I
C ACID DECARBOXYLASE (
                                                         Similarity
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00282; pyridoxal_deC; 2.
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370 AA;
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370 2
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larity 75.0%;
Conservative
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63.2%;
                                                                                                           30264 MW;
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Pred. No. 5
3; Mismat
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Pred.
3; M
                                  Score 113; DB 4;
Pred. No. 2.33e-12;
6; Mismatches 1
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                                                                                                               A3475A7D CRC32;
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1. No. 5.61e-15;
1. No. 5.61e-2;
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No. 5.61e-15;
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3J databases.
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Q64577;
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Q1-NOV-1999
Q1-NOV-1999
CYSTEINE SUL
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EMBL; U74492; AAB18332.1; -.
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Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70713 PRELIMINARY; PRT; 78 AA.
P70713;
P70713;
O1-FEB-1997 (TrEMBLrel. 02, Created)
O1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
O1-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)
CSULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE
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"Human cysteine sulfinic acid decarboxylase ('
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ
EMBL; AF116547; AAD32545.1; -
SEQUENCE 493 AA; 54951 MW; F4852742 CRC32
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PRITCHARD J.E.,
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Entheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYSTEINE
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota: Metazoa: Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                       37
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::|::|||||:||:||:|
2 LKYAIKTGHPRYFNQLSTG
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12; Conservative
                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                          Similarity
996 (TrEMBLrel. 01, Created)
996 (TrEMBLrel. 01, Last sequence update)
999 (TrEMBLrel. 12, Last annotation update)
999 (TrEMBLrel. 12, Last annotation update)
SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)
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999 (TremBirel. 12, Last sequence update)
999 (TremBirel. 12, Last annotation update)
999 (TremBirel. 12, Last annotation update)
SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa;
Rodentia;
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Primates; Catarrhini; Hominidae;
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78
7 AA;
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                                                                                                                  PRELIMINARY;
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78
9134 MW;
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63.28;
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63.2%;
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Pred. No. 4.48e-11;
5; Mismatches 2
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No. 2.33e-12;
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HYPOTAURINE
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Rattus.
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Matches
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O64611;

O64611;

O1-NOV-1996 (TremBLrel. O1, Created)

O1-NOV-1996 (TremBLrel. O2, Last sequence update)

O1-NOV-1996 (TremBLrel. 12, Last annotation update)

CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)

CYSTEINE SULFINATE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
11
Q9XTP4
Q9XTP4;
Q9XTP4;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: YOLD ON TAPPAZ M.;
REYMOND I., SERGEAUT A., TAPPAZ M.;
"Molecular cloning and sequence analysis of the cDN?
liver cysteine sulfinate decarboxylase (CSD).";
Biochim. Biophys. Acta 1307:152-156(1996).
- COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
- COPACTOR: BELONGS TO GROUP II DECARBOXYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00392; DDC_GAD_HDC_YDC; PFAM; PF000282; pyridoxal_dec; 1. Lyasse; Decarboxylasse; Pyriboxal phosequence 478 AA; 53725 MW; 4CAV
                                                                                                                                                                                                                                                                                                      PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_dec; 1.
Lyasse; Decarboxylasse; Pyridoxal phosphate.
SEQUENCE 493 AA; 55248 MW; D7A66D9A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE). Rattus norvegicus (Rat). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X94152; CAA63868.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M64755; AAC42063.1;
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"Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                           Match
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CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE - HYPOT COFACTOR: PYRIDOXAL-PHOSPHATE.
COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
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                                                                                                                               LKYAIKTGHPRYFNQLSTG
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Similarity 63.2%;
12; Conservative
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12; Conse
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                                           PRELIMINARY;
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na; Chordata; Craniata; Vertebrata;
.a; Sciurognathi; Muridae; Murinae;
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Pred.
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Pred.
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4CAC0093 CRC32;
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1. No. 4.48e-11;
Mismatches 2;
                                                                                                                                                                                                               e 108; DB 11; LG. NO. 4.48e-11; LG. 2;
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No. 4.
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nic acid
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RESULT ACCOUNTS OF THE SOLUTION OF THE SOLUTIO
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GLUTAMIC ACID DECARBOXYLASE.
UNC-25 OR Y37D8A.23.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                024062:
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLUTAMATE DECARBOXYLASE.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
                                               PFAM; PFC
SEQUENCE
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Q24062
Q24062;
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CORATTON M., DEAR S., DU Z., DURBIN R., FAPELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JCNES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL:
MEDLINE, 99098940.
JIN Y., JORGENSEN E., HARTWIEG E., HORVITZ H.R.;
"The Caenorhabditis elegans gene unc-25 encodes;
decarboxylase and is required for synaptic transf
synaptic development.";
J. Neurosci. 19:539-548(1999).
                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
EMBL; AF109378; AAD19958.1; -.
EMBL; AL023626; CAA21537.1; -.
SEQUENCE 508 AA; 57792 MW; · 3A3E7F33 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=C.elegans; MEDLINE; 94150718.
                                                                                                                                                             STRAIN=OREGON-R; TISSUE=NEURAL; PHILLIPS M., SALKOFF L., KELLY
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila
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                                                                                                 YBASE;
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                                                                                                                     Neurochem. 0:0-0(0).
%L; U01239; AAC46466.1;
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                                             se; FBgn0005622; Gad2.
PF00282; pyridoxal_deC;
NCE 575 AA; 64795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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57.9%;
  59.28;
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6; M
  Score
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3CFA48E5 CRC32;
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  87;
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No. 4.48e-08
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  DB
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  575;
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but not
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RESULT 15
ID 029449;
AC 029449;
DT 01-NOV-1996 (
DT 01-JAN-1999 (
DT 01-JAN-1999 (
DT 01-GRY-1996 (
DE CHROMAFFIN GI
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ID Q9W668;
AC Q9W668;
DT 01-NOV-1999
DT 01-NOV-1999
DF MATRIX GLA PB
GN MGP.
OS Xenopus laevi
OC Eukaryota; Me
OC Eukaryota; Me
OC Eukartotia; An
OC Xenopus.
RN [1]
RP SEQUENCE FROM
RA CANCELA M.L.;
Submitted (MA
DR EMBL; AF05558
FT NON_TER
SQUENCE 77
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AC 044
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043308;
01-JUN-1998
01-JUN-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1998) to the EMBL; AF055588; AAD28354.1; NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANAKA A., KOTANI H., NOMURA Submitted (OCT-1997) to the EMBL; AB007885; BAA24855.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAAU422.
Homo sapiens (Human).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1089 TLKYSTKMTYLRFFPPL 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. CANCELA M.L.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISHIKAWA K., NAGASE T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 TIRFSVKTGHPYFINQLYSG
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Similarity 47.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                     Similarity
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96 (TremBLrel. 01, 99 (TremBLrel. 09, 99) (TremBLrel. 10, 99) (TremBLrel. 10, N GRANULE ATPASE II
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
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                                                                                                           PRELIMINARY;
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8; M
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2; M
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EMBL/GenBank/DDBJ
                                                                 Created)
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i; Hominidae;
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                                                                                                                                                                                                                                                                                 Mismatches
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. 1.11e-01;
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                                                                                                                                                                                                                                                                                                                      DB 13;
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                                                                                                                                                                                                                                                                                                                      Length
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OS Bos taurus (Bovine).

OC Eutheryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Bovinae; Metazoa; Chordata; Ruminantia; Peccora; Bovoidea; Bovidae;

OC Bovinae; Bos.

RN [1]

RN [2]

RN [3]

RN [1]

RN [1]

RN [1]

RN [1]

RN [2]

RN [1]

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|-----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|----------------------|-----------------------|-----------------------|-----------------------|------------|-----------------------|----------|-----------------------|
| 60                    | 60                    | 60                    | 61                   | 61                   | 61                    | 61                    | 61                    | 61                    | 61                    | 61                    | 61                    | 61                    | 61                    | 61                   | 62                    | 62                    | 62                    | 62         | 62                    | 63       | 64                    |
| 38.7                  | 38.7                  | 38.7                  | 39.4                 | 39.4                 | 39.4                  | 39.4                  | 39.4                  | 39.4                  | 39.4                  | 39.4                  | 39.4                  | 39.4                  | 39.4                  | 39.4                 | •                     |                       | 40.0                  | 40.0       | 40.0                  | 40.6     | 41.3                  |
| 1578                  | 1471                  | 1375                  | 661                  | 538                  | 463                   | 463                   | 463                   | 463                   | 455                   | 454                   | 453                   | 453                   | 360                   | 216                  | 575                   | 552                   | 407                   | 344        | 294                   | 409      | 796                   |
| ۵                     | N                     | N                     | N                    | Н                    | N                     | N                     | N                     | N                     | 2                     | Н                     | N                     | 2                     | 2                     | N                    | <u></u>               | N                     | N                     | N          | 2                     | N        | 2                     |
| 148216                | B48218                | F48216                | S75005               | D64164               | S39925                | S39926                | A40013                | S33528                | S46316                | XNYLB                 | S39928                | S39927                | S58205                | S58652               | JH0827                | JQ1193                | JC5124                | H64477     | D70525                | S53303   | A45695                |
| neurexin III-alpha me | neurexin III-alpha me | neurexin III-alpha se | sensory transduction | hypothetical protein | aspartate transaminas | aspartate transaminas | phosphomannomutase (E | aspartate transaminas | DHR38 protein - silkw | hypothetical protein | glutamate decarboxyla | cholesterol oxidase ( | aspartate transaminas | ehydrogena | probable beta-1 - Myc | œ        | capsid precursor - hu |
| 2.78e+01              | 2.78e+01              | 2.78e+01              | 1.93e+01             | 'n                   | 1.93e+01              | 1.93e+01              |                       | 1.93e+01              | 1.93e+01              | 1.93e+01              |                       |                       | 1.93e+01              | 1.93e+01             | 1.33e+01              | 1.33e+01              | 1.33e+01              | 1.33e+01   | 1.33e+01              | 9.16e+00 | 6.27e+00              |

# ALIGNMENTS

| ١.                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                          |                                         |                                                                                                                                                         |                                                                                                                                                                                                                                  |                                                                                                                                                                                                                |                                                                                                                       |                                                                                                                                                                                                       |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| #journal #title #cross-referen #accession #amolecule_                                                                                                                                                                                                                | RESULT 2 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE                                                                                                                                                                                                  | Db 2 PRYFNQI<br>       <br>Qy 1 PRYFNQI | Query Match<br>Best Local Simi<br>Matches 20;                                                                                                           | ##status<br>##molecule<br>##residues<br>##cross-ref<br>CLASSIFICATION<br>SUMMARY                                                                                                                                                 | eferen<br>on                                                                                                                                                                                                   | ACCESSIONS REFERENCE #authors #journal                                                                                | RESULT 1 ENTRY TITLE ORGANISM DATE                                                                                                                                                                    |
| <pre>#authors Erlander, M.G.; Tillakaratne, N.J.K.; Feldblum, S.; Patel,     N.; Tobin, A.J. #journal Neuron (1991) 7:91-100 #title Two genes encode distinct glutamate decarboxylases. #cross-references MUID:91299343 #accession JH0423 ##molecule_type mRNA</pre> | JH0423 #type complete glutamate decarboxylase (EC 4.1.1.15) 2 - rat glutamate decarboxylase GAD55; L-glutamate 1-carboxy-lyase #formal_name Rattus norvegicus #common_name Norway rat 31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999 JH0423; A60888 | PRYENQLSTGLDMYGLAADW 21<br>             | y Match 100.0%; Score 155; DB 2; Length 205;<br>Local Similarity 100.0%; Pred. No. 3.18e-19;<br>hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | ##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA ##residues 1-205 ##label RES ##coss-references GB:S67454; NID:g456852 ##CTCATION #superfamily human glutamate decarboxylase Y #length 205 #checksum 3167 | title Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat. cross-references MUID:94062679 accession 167412 | <pre>167412 153274 Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harrison, L.C. Endocrinology (1993) 133:2962-2972</pre> | 167412 #type fragment 65 kda glutamate decarboxylase, brain - mouse (fragment) #formal_name Mus musculus #common_name house mouse 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 30-May-1997 |

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 Matches
 **TRENCE A60888, Y.C.; Gottlieb, D.I.

#authors Chang, Y.C.; Gottlieb, D.I.

#journal J. Neurosci. (1988) 8:2123-2130

#title Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.

#cross-references_MQID:88258610
 #authors Karlsen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes,
Grant, F.J.; Foster, D.; Lernmark, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
Cloning and primary structure of a human islet isoform c
#title glutamic acid decarboxylase from chromosome 10.
#cross-references_MUID:92020848
 #authors
 #cross-references MUID:92196068
 #journal
 #accession
 #accession
 #accession
 ##molecule_type protein

'V', 191-194,'X',196-203,'XX',206-219;'X',225-234,'X',

##residues

'V', 191-194,'X',249-266,'X';524-537,539-543,'V',547-549,

236-247,'X',249-266,'X';524-537,539-543,'V',547-549,

"X',551-553,'X',555-558 ##label CHA

'X',551-553,'X',555-558 ##label CHA

"This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
 ##experimental_source
 ##molecule_type mRNA
 ##note
 ##experimental_source brain
 ##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
 ##residues
 176 PRYFNQLSTGLDMVGLAADW 195
 ##experimental_source brain
 ##residues 1-585 ##label ERL ##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
 ##molecule_type mRNA
 Local
 1 PRYFNQLSTGLDMVGLAADW 20
 ω
 h 100.0%;
Similarity 100.0%;
20; Conservative
 Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.
 glutamate decarboxylase (EC 4.1.1.15) 2 - human glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Homo sapiens #common_name man 13-May-1992 #sequence_revision 23-Mar-1995 #text_change
 A60888
 A41935
 Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;
Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
 A41292
 A41935; A41292; S30058; B54778
 #length
 A41935
 phosphate
 18-Jun-1999
 ource prain
the authors translated the
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
 preliminary
 sequence extracted from NCBI backbone (NCBIP:88007)
 1-585 ##label BU1
 428 as Trp
 585
pancreatic islet
 #type complete
 #molecular-weight 65402
 Score 155; DB 1; Length 585; Pred. No. 3.18e-19;
 0;
 Mismatches
 codon GAT for residue 86 as as Ala, and CAG for residue
 0;
 #checksum
 Indels
 0
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 0
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#map_position CLASSIFICATION
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 #contents annotation; intron-exon boundaries

MMENT This enzyme (GAD) catalyzes the formation of an inhibitory

neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;

it has several isoforms, each encoded by a separate gene. GAD has

also been implicated as an autoantigen in autoimmune disease
 #journal #title
 #accession
 #cross-references MUID:93185681 #accession $30058
 #cross-references MUID:94032481
 #journal
 #gene
 #cross-references MUID:94375018
 #title
 #journal
 #authors
 #authors
 authors
 ##residues 1-585 ##label LEE
##cross-references GB.L16580; NID:g413867; PIDN:AAA93049.1; PID:g413868
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
 176 PRYFNQLSTGLDMVGLAADW 195
 ##experimental_source pancreatic islet
NCE A54778
 ##molecule_type mRNA
 ##cross-references GDB:128595; OMIM:138275
 ##cross-references EMBL:X69936
 ##residues
 ##status
 #molecule_type mRNA
 ۳
 PRYFNQLSTGLDMVGLAADW
 h 100.0%;
Similarity 100.0%;
 stiff-man syndrome and insulin-dependent diabetes mellitus
it has several isoforms, each encoded by a separate gene.
N #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 938533 #type complete glutamate decarboxylase (EC 4.1.1.15) 2 - mouse glutamate decarboxylase (EC 4.1.1.15) 2 - glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Mus musculus #common_name house mouse #CO-May-1994 *sequence_revision 23-Mar-1995 #text_change
 S38533
S38533
 10p11.23-10p11.23
#superfamily human glutamate decarboxylase family human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 Eur. J. Biochem. (1993) 212:597-603
Characterization of a linear epitope within the human pancreatic 64-KDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
#length 585 #molecular-weight 65/11 #____
 Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.
Biochim. Biophys. Acta (1993) 1215:157-160
Cloning and sequence analysis of a murine cDNA encoding
glutamate decarboxylase (GAD65).
 Genomics (1994) 21:222-228

The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral
 S38533
 GDB:GAD2
 Bu, D.F.; Tobin, A.J
 Mauch,
 S30058
 Conservative
 GAD
 B.; Northemann,
 phosphate
 18-Jun-1999
 6-585 ##label MAU
 preliminary
 L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
Northemann, W.
 20
 Score 155; DB 1;
Pred. No. 3.18e-19;
0; Mismatches 0
 ò
 Length 585;
 Indels
 0
 Gaps
 0
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 #journal
#title
 #journal
#title
 stop codon in t
#cross-references_MUID:91062362
 #authors
 #cross-references MUID: 95137399
 #accession
 #authors
 ##experimental_source brain
This enzyme catalyzes the conversion of glutamic gamma-amino butyric acid.
FICATION #superfamily human glutamate decarboxylase
 ##residues 1-585 ##label SUZ ##cross-references DDBJ:D31848; NID:g790964; PIDN:BAA06635. ##cross-references DDBJ:d1007207; PID:g790965
##residues 1-223 ##label RES
1-223 ##label RES
##cross-references GB:M38350; NID:g204231; PIDN:AAA41185.1; PID:g204232
FICATION #superfamily human glutamate decarboxylase
XY #length 223 #molecular-weight 25069 #checksum 1388
 176 PRYFNQLSTGLDMVGLAADW 195
 176 PRYFNQLSTGLDMVGLAADW 195
 ##molecule_type mRNA
 ##status
 y Match 100.0%;
Local Similarity 100.0%;
 ##molecule_type mRNA
 y Match 100.0%;
Local Similarity 100.0%;
hes 20; Conservative
 μ
 \vdash
 σ
 PRYFNQLSTGLDMVGLAADW 20
 PRYFNQLSTGLDMVGLAADW 20
 20;
 Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775
Developmentally regulated expression of an exon containing
stop codon in the gene for glutamic acid decarboxylase.
 Suzuki, R.; Asami, N.; An
Gene (1995) 152:257-260
Sequences of two porcine
 JC4064
 #formal_name Rattus norvegicus #common_name Norway rat
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
22-Jun-1999
 glutamate decarboxylase - rat
 #length 585
 carbon-carbon lyase; carboxy-lyase
 I59173
 JC4064
 glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig
#formal_name Sus scrofa domestica #common_name domestic pig
30_Jun-1995 #sequence_revision 14-Jul-1995 #text_change
 #length 585
 159173
 Conservative
 67-kDa GAD)
 22-Jun-1999
 phosphate
 #domain DOPA decarboxylase binding #status
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
 preliminary; translated from GB/EMBL/DDB.
 #label BIN
 #type complete
 #type complete
 #molecular-weight 65388
 #molecular-weight 65224 #checksum
 Score 155; Ub ...
bred. No. 3.18e-19;
 Pred.
 Score 155; DB 1;
Pred. No. 3.18e-19;
 Mismatches
 Amann, E.; Wagatsuma, M
 glutamic acid decarboxylases (65-and
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 Length 585;
 Length 585;
 #checksum
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 #accession
 #submission
 #accession
 #cross-references MUID:92020930
 #journal
 #authors
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 #authors
 #authors
##residues 1-593 ##label MIC
##cross-references GB:M75177; NID:9204227; PIDN:AAA41184.1;
 184 PRFFNQLSTGLDIIGLAGEW 203
 ##cross-references EMBL:249976; NID:g886686; PID:g886687
 ##experimental_source brain
 ##residues 1-585 ##label KAT
##CIOSS-references EMBL:Z49976
 ##molecule_type mRNA
 ##note
 ##experimental_source brain
 ##molecule_type mRNA
##residues 1-554,'YQPQGDKANFFRMYISNPAASQSDIDFLTEEIERLGQDL'
 184 PRFFNQLSTGLDIIGLAGEW 203
 Match 87.18; Local Similarity 75.08;
 ##molecule_type mRNA
 ||:||||||||::|||::|
PRYFNQLSTGLDMVGLAADW
 œ
 PRYFNQLSTGLDMVGLAADW 20
 h 87.1%;
Similarity 75.0%;
 15;
 15;
 glutamate decarboxylase (EC 4.1.1.15) 1 - rat
glutamate decarboxylase GAD57; L-glutamate 1-carboxy-lyase
#formal_name Rattus norvegicus #common_name Norway rat
12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
 A41367
 Cloning, characterization, and autoimmune recognition of islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
 submitted to the EMBL Data Library, {\tt S61533}
 Katarova, 2.; Szabo, G.; Mugnaini, E.;
Eur. J. Neurosci. (1990) 2:190-202
Molecular identification of the 62 kd decarboxylase from the mouse.
 glutamate decarboxylase (EC glutamic acid decarboxylase
 Dyrberg, T.; Madsen, O.D. Proc. Natl. Acad. Sci. U.S.A.
 Michelsen,
 S61534
 #formal_name Mus musculus #common_name house
19-Mar-1997 #sequence_revision 25-Apr-1997 #t
22-Jun-1999
 А41367; А43756; ЈН0195
 Szabo, G.
 S61534; S61533
 Conservative
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 preliminary
 the differences at the carboxyl end are
 SZA
 B.K.; Petersen,
 #type complete
 #type complete
 20
 Score 135; DB 2;
Pred. No. 1.57e-14;
 Pred.
 Score 135; DB 2;
Pred. No. 1.57e-14;
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 Mismatches
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 J.S.; Boel,
 4.1.1.15) 62K isoform -
 (1991) 88:8754-8758
 PIDN: CAA90277.1;
 0
 Length 585;
 0
 Length 223;
 June 1995
 Indels
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 E.; Moldrup,
 Greenspan, R.J.
 of glutamic acid
 #text_change
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 PID: g204228
 Gaps
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 ##label
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 #journal
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 cloned cDNA.
#cross-references MUID:90132703
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 #cross-references MUID:91014554
 #title
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 #authors
 decarboxylase.
cross-references MUID:93080286
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 ##CTOSS references EMBE: 22750

##CTOSS references EMBE: 22750

##Superfamily human glutamate decarboxylase

RDS carbon-carbon lyase; carboxy-lyase

RY #length 593 #molecular-weight 66952 #chec
 ##residues 1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',
348-351,'LE',354-379,'R',381-593 ##label JUL
##cross-references GB:X57572; NID:956185; PIDN:CAA40800.1; PID:956186
NT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
#superfamily human glutamate decarboxylase
RDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 ##molecule_type mRNA
1-593 ##label WYB
1-593 ##label WYB
##cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184
##cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184
##note the authors translated the codon TGT for residue 412
Ser and TCT for residue 413 as Cys
 ##residues
 184 PRFFNQLSTGLDIIGLAGEW 203
184 PRFFNQLSTGLDIIGLAGEW 203
 ##molecule_type mRNA
 ##molecule_type mRNA
 Local
 Local
 1 PRYFNQLSTGLDMVGLAADW 20
 h 87.1%;
Similarity 75.0%;
15; Conservative
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 JH0195
 Julien, J.F.; Samama, P.; Mallet, J. Neurochem. (1990) 54:703-705
 A43756
 A43756
Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.
Brain Res. Mol. Brain Res. (1990) 8:193-198
 Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.; Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D. Ann. Hum. Genet. (1992) 56:255-265

Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate
 glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo sapiens #common_name man
14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
 Rat brain glutamic acid decarboxylase sequence deduced from
 Characterization of a
 S48135
 S48135
 #length
 Conservative
 07-May-1999
 phosphate
 1-593 ##label KEL
 #binding_site pyridoxal phosphate (Lys) (covalent)
 #status predicted

jth 593 #molecular-weight 66640 #checksum 3971
 preliminary
 87.1%;
75.0%;
 #type complete
 Score 135; DB 1;
Pred. No. 1.57e-14;
5; Mismatches (
 Pred.
 Score 135;
Pred. No. 1
 Mismatches
 cDNA coding for rat glutamic acid
 DB 2; Length 593; .57e-14;
 0;
 Length 593;
 Indels
 #checksum
 Indels
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 Query Match 87.1%;
Best Local Similarity 75.0%;
Matches 15; Conservative
 Kawasaki, E.; Moriuchi, R.; Watanabe, M.; Saitoh, K.; Chi
Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;
Akazawa, S.; Miyamoto, T.; Nagataki, S.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
"title Cloning and expression of large isoform of glutamic acid
decarboxylase from human pancreatic islet."
 #accession
 #cross-references MUID:92196068
 #journal
 #authors
 #accession
 #submission
 #authors
 ##molecule_type mRNA
1-17,'N',19-30,'N',32-67,'K',69-115,'L',117-154,'T',
##residues 156-301,'C',303-476,'G',478-491,'G',493-594 ##label
 184 PRFFNQLSTGLDIIGLAGEW
 ##experimental_source pancreatic
 ##cross-references GB:S61898; NID:g385310;
##experimental_source pancreatic islet
 ##cross-references EMBL: 222750
 ##residues
 ##molecule_type mRNA
 ##status
 1 PRYFNQLSTGLDMVGLAADW 20
 1 PRYFNQLSTGLDMVGLAADW
 11
 10
 glutamate decarboxylase (EC 4.1.1.15) 1 - human glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase #formal_name Homo sapiens #common_name man 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
 *superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase
 glutamate decarboxylase (EC 4.1.1.15) - human #formal_name Homo sapiens #common_name man 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Feb-1997
 submitted to the
 B41935
 Two human glutamate decarboxylases, 65-kDa GAD, are each encoded by a single gene.
 Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin
 В41935; JH0805; JH0806; A61406; PQ0157; PQ0158; B41367;
 S51776
 Johnstone,
 S51775
 Proc. Natl. Acad.
 A41935
 #length 593
 Yamashita,
 18-Jun-1999
 A36463; A54778
 this is an unpublished revision to the sequence from reference {\tt S48135}
 1-593 ##label
 preliminary
 sequence extracted from NCBI backbone (NCBIP:88006)
K.; Cram,
 #type complete
 #type complete
 #molecular-weight 66946
 203
 20
 Score 135; DB 2;
Pred. No. 1.57e-14;
5; Mismatches 0
 EMBL Data Library,
 sci. U.S.A. (1992) 89:2115-2119
 JOH
 PIDN:AAB26938.1; PID:g385311
 Length 593;
 Indels
 #checksum
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COMMENT
 REFERENCE
 ##experimental_source pancreatic islet
REFERENCE A41367
 REFERENCE
 REFERENCE
GENETICS
 REFERENCE
 S.; Skog, S.; Hockfelt, T.; Ritzen, E.M.

*Litle Expression of the neurotransmitter-synthesizing glutamic acid decarboxylase in male germ cells #cross-references MUID:90355986
 #journal
#title
 #authors Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C. #journal Blochem. Biophys. Res. Commun. (1991) 176:1239-1244

Blochem. Biophys. Res. Commun. (1991) 176:1239-1244

#title Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets. #cross-references MUID:91248209
 #authors
#journal
#title
 #cross-references MUID:92065769
#accession A61406
 #contents
 #cross-references MUID:94375018
 #accession
 #cross-references MUID:92020930
 #title
 #journal
 #authors
 #accession
 #accession
 #journal
 #authors
 #accession
 #accession
 #cross-references MUID:93282844
 ##residues
 ##molecule_type mRNA
##residues 527-594 ##label PER
##cross-references GB:M55574; NID:g182929; PIDN:AAA72938.1;
 ##molecule_type mRNA

##residues 218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,

'D',331-338,'L',340-390,'S',392-397 ##label CR2

##cross-references GB:M70435; NID::182941; PIDN:AAA52513.1; PID::g182942
 ##experimental_source brain
 ##molecule_type mRNA
 ##experimental_source brain
 ##residues 218-463 ##label
##cross-references GB:M70434
 ##residues
 ##experimental_source pancreatic islet
NCE A61406
 ##molecule_type mRNA
 ##molecule_type mRNA
##residues 62-67,'K',69-205,'N',207-564,'L',566-594 ##label
 This enzyme (GAD) catalyzes the formation of
 also been implicated as stiff-man syndrome and
 neurotransmitter,
 urotransmitter, gamma-aminobutyric acid, from L-glutamic acid; has several isoforms, each encoded by a separate gene. GAD has so been implicated as an autoantigen in autoimmune disease iff-man syndrome and insulin-dependent diabetes mellitus.
 Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyrberg, T.; Madsen, O.D.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
Cloning, characterization, and autoimmune recognition of islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
 Bu, D.F.; Tobin, A.J.

Genomics (1994) 21:222-228

The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral
 Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S. Lancet (1991) 338:1468-1469
Cloning of large isoform of human brain glutamic acid decarboxylase.
 Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
Molecular cloning of full-length glutamic acid decarboxylase
67 from human pancreas and islets.
 A36463
 Persson, H.; Pelto-Huikko, M.; Metsis,
 A36463
 B41367
 JH0806
 317-482,'R',484-594 ##label MIC
 CR1
 an inhibitory
 cells.
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 #map_position CLASSIFICATION
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 Matches
 Best Local Similarity
 Query Match
 Matches
 Query Match 87.1%;
Best Local Similarity 75.0%;
 #authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal J. Neurosci. (1987) 7:2768-2772
#title Glutamic acid decarboxylase cDNA: nucleotide sequence
encoding an enzymatically active fusion protein.
#cross-references_MUID:87310623
 #accession A45/58
##molecule_type mRNA
 405
 #accession
 #submission
 #authors
 #accession
 #submission
 #authors
 ##residues 1-594 ##label KOB
##cross-references GB:M18629; NID:g163858; PIDN:AAA51430.1; PID:g163859
ENCE A45671
 185 PRFFNQLSTGLDIIGLAGEW 204
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1-558,'RGTRPTFSGWSSRTQLLHSPILTSSSRR'
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PID:9298099
PID:9298099
#Superfamily human glutamate decarboxylase
the carbon-carbon lyase; carboxy-lyase
 ##residues
 ##molecule_type mRNA
 ##cross-references GDB:119244; OMIM:266100
 ##status
 1 PRYFNQLSTGLDMVGLAADW
 1 PRYFNQLSTGLDMVGLAADW
 13
 12
 glutamate decarboxylase (EC 4.1.1.15) 1 - cat
glutamate decarboxylase GAD57; L-glutamate 1-carboxy-lyase
#formal_name Felis silvestris catus #common_name domestic of
31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
 #superfamily human glutamate decarboxylase alternative splicing; carbon-carbon lyase; phosphoprotein; pyridoxal phosphate
 A45671
 Kobayashi, Y.; Kaufman, D.L.; Tobin, submitted to GenBank, September 1989
 $51775 #type complete
glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo sapiens #common_name man
15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
 A46758; A45671°
A46758
 Johnstone, A. submitted to the
 2q31-2q31
 A46758
 #length 594 #molecular-weight 66973 #checksum
 S51775
 S51775
 #length
 GDB:GAD1;
 Conservative
 Conservative
 18-Jun-1999
 22-Jun-1999
 1-594 ##label JOH
 preliminary
 #binding_site pyridoxal phosphate (Lys) (covalent)
 87.1%;
75.0%;
 #status predicted
 594 #molecular-weight 66924 #checksum
 GAD
 #type complete
 Score 135; DB 2;
Pred. No. 1.57e-14;
 Score 135; DB 1;
Pred. No. 1.57e-14;
 EMBL Data Library,
 Mismatches
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 Length 594;
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 lyase;
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 ##label KO2
 carboxy-lyase;
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COMMENT

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 commental source brain this enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.

CLASSIFICATION #superfamily human glutamate decarboxylase
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 #authors #journal
 Matches
 #journal
#title
 #accession JC4vvo
##molecule_type mRNA
 405
 #title
 402-405
 *cross-references MUID:95137399
 #authors
 185 PRFFNQLSTGLDIIGLAGEW 204
 ##residues 1-594 ##label SUZ
##cross-references DDBJ:D31849; NID:g790966; PIDN:BAA06636.1;
PID:d1007208; PID:g790967
 ##note this sequence has been revised in reference A46758
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
 185 PRFFNQLSTGLDIIGLAGEW 204
 Local
 ب
 1 PRYFNQLSTGLDMVGLAADW 20
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 15
 ||:|||||||::|||::|
PRYFNQLSTGLDMVGLAADW 20
 h 87.1%;
Similarity 75.0%;
15; Conservative
 (Drosophila melanogaster)
L-glutamate 1-carboxy-lyase
#formal_name Drosophila melanogaster
26-Oct_1989 #sequence_revision 23-Mar-1995
 Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M. Gene (1995) 152:257-260
Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).
 JC4065
JC4064
 glutamate decarboxylase (EC 4.1.1.15) 67K chain - pig #formal_name Sus scrofa domestica #common_name domestic 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 22-Jun-1999
 Jackson, F.R.; Newby, L.M.; Kulkarni, J. Neurochem. (1990) 54:1068-1078
 A30999 #type complete glutamate decarboxylase (EC 4.1.1.15)
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
#length 594 #molecular-weight 66824 #checksum 5630
 #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 JH0192; PS0301; A30999
 #length 594
 carbon-carbon lyase; carboxy-lyase
 GADI
Drosophila GABAergic systems; sequence and expression
 Conservative
 18-Jun-1999
 phosphate
 \begin{tabular}{ll} $\# domain DOPA decarboxylase binding $\# status predicted \\ $\# label BIN \end{tabular}
 87.1%; score 135; DB 2; Length 594; 75.0%; Pred. No. 1.57e-14;
 #type complete
 #molecular-weight 66894 #checksum 5491
 Pred.
5; M
 Score 135; DB 1; Length 594; Pred. No. 1.57e-14; 5; Mismatches 0; Indels
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 #text_change
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 #accession
 glutamic acid decarboxylase.
#cross-references_MUID:90155291
 #gene
 #accession
 ##molecule_type mRNA
156-200,'F',202-300,'K',302-384,'L',386-510 ##label JA2
#Tris enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
 ##residues 1-510 ##label JAC
##cross references GB:X76198; NID:g433082; PIDN:CAA53791.1; PID:g433083
ccession PS0301
 102 PHFENQLSNGLDLISMAGEW 121
 ##molecule_type mRNA
##residues 1-51
 ##cross-references FlyBase:FBgn0004516
FICATION #superfamily human glutamate decarboxylase
Carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 1 PRYFNQLSTGLDMVGLAADW 20
 h 74.2%;
Similarity 55.0%;
 JH0192
 #status predicted
#length 510 #molecular-weight 57758
 FlyBase:Gadl
 Conservative
 phosphate
 #binding_site pyridoxal phosphate (Lys) (covalent)
 7 21:43:54 2000
 Score 115; DB 1;
Pred. No. 5.13e-10;
8; Mismatches 1
 Length 510;
 Indels
 #checksum 3194
 Gaps
 0,
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444440333333337754

YCR2\_ERWHE
SYL\_SYNY3
MIH\_CANMG
BIOD\_ERWHE
PRAI\_CANNG
HTGTJA
CATT\_PIG
PAGI\_SHEEP
FD62\_SOVEN
AATT\_MEDSA
AATI\_MEDSA
AATI\_MEDSA
AATI\_MEDSA
AATI\_MEDSA
AATI\_SHEEP
YC36\_HAEIN
Y 254\_HAEIN
Y 254\_

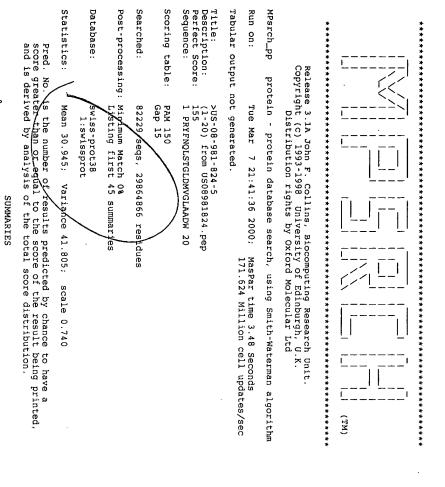
DETHIOBICTIN SYNTHETAS
PH-REGULATED ANTIGEN P
PUTATIVE TRANSKETOLASE
CATHEPSIN D (EC 3 .4.23
PREGNANCY-ASSOCIATED G
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HYPOTHETICAL ARGINYL-TRNA

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ALIGNMENTS

| Similarity 1<br>20; Conserv                                                                       | EMBL; M7242; AAA63488.  PROSITE; PS00392; DDC_G  PFAM; PF00282; Pyridoxa  Neurotransmitter blosyn  Neuridoxal phosphate; Mu  BINDING 396 396  SFOURTE 58 AA 65 | This SWIS between the Europ use by modified entities or send                                                                           | RP SEQUENCE FROM N.A.  RC TISSUE-HIPPOCAMPUS;  RX MEDLINE; 91299343.  RA ERLANDER M.G., TILLAKARATNE N.J., FELL  RA TOBIN A.J.;  RT "Two genes encode distinct glutamate of the company of the production of the prod | DCE2_RAT  OCES_RAT  OCES_RAT  OCES_CONTROL   |
|---------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| %; Score 155; DB 1; Length 585;<br>%; Pred. No. 2.36e-21;<br>e 0; Mismatches 0; Indels 0; Gaps 0; | YDC; 1. 1. Lyase; Decarboxylase; family, YRIDOXAL PHOSPHATE (POTENTIAL P35D601A CRC72:                                                                         | iced through a collabor and the EMBL outstat are no restrictions on its content is in no sage by and for comme p://www.isb-sib.ch/anno | UE-HIPPOCAMPUS; INE; 9129343.  INE; 9129343.  NDER M.G., TILLAKARATNE N.J., FELDBLUM S., PATEL N.,  N.A.J.;  N.A.J.;  OR A.J.;  OR J.91-100(1991).  FUNCTION: CATALYZES THE PRODUCTION OF GABA.  CATALYTIC ACTIVITY: LGLUTANATE = 4-AMINOBUTANOATE + CO(2).  COFACTOR: PYRIDOXAL PHOSPHATE.  SUBUNIT: HOMODIMER (BY SIMILARITY).  SUBUNIT: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  DECARBOXYLASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | DARD; PRT; 585 AA.  3, Created) 3, Last sequence update) 3, Last annotation update) 1, Last annotation (EC 4.1.1.15) (GAD-65) 1, Last sequence update) 1, Last sequence update u |

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PROBABLE TRANSCRIPTION CYTOCHROME B561 (CYTOC

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Q1-FEB-1996 (Rel. 33, East annotation update)
Q1-FEB-1996 (Rel. 33, East Annotation update)
Q1-FEB-1996 (Rel. 33, East Annotation update)
 DCE2_PIG
P48321;
 MEDLINE;
BU D.-F.,
 use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; Pyridoxal_dec; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
 01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.
(55 KD GLUTAMIC ACID DECARBOXYLASE).
 DCE2_
 MEDLINE; 95137399.
SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
"Sequences of two porcine glutamic acid deca
67-kDa GAD).";
Gene 152:257-260(1995).
 Eutheria;
 Eukaryota;
 EMBL; D31848; BAA06635.1; -. PROSITE; PS00392; DDC_GAD_HI
 Eutheria;
 Eukaryota; Metazoa;
 Sus scrofa (Pig)
 01-FEB-1996
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 FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE +

COFACTOR: PYRIDOXAL PHOSPHATE.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC,
 s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict the contract of the
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 PRYFNQLSTGLDMVGLAADW 195
 OR GAD65
 PRYFNQLSTGLDMVGLAADW
 h 100.0%;
Similarity 100.0%;
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 ; Metazoa; Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae; Sus.
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NTNG 65411 MW;
 PROSITE: ES00392; DDC_GAD_HDC_YDC; 1.

PROM; PF00282; pyridoxal_deC; 1.

Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.

BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
 -i- FUNCTION: CATALYZES THE PRODUCTION OF GAI-
-i- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMING
-i- COFACTOR: PYRIDOXAL PHOSPHATE.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE,
 64-kDa glutamic acid decarboxylase and its aut sera from insulin-dependent diabetes mellitus Eur. J. Biochem. 212:597-603(1993).
 SEQUENCE FROM N.A. TISSUE-PANCREATIC ISLETS;
 "The exon-intron organization of the genes two human glutamate decarboxylases (GAD67 they derive from a common ancestral GAD."; Genomics 21:222-228(1994).
 WAGNER-MCPHERSON C.B., EVANS G.A., TO "TWO human glutamate decarboxylases, each encoded by a single gene "; proc. Natl. Acad. Sci. U.S.A. 89:2115
 EMBL;
 or send
 the European Bioinformatics Institute.
 This SWISS-PROT entry is copyright. between the Swiss Institute of Bio:
 NORTHEMANN W.;
 MAUCH L., ABNEY C.C.,
 MEDLINE; 93185681.
 TISSUE-PANCREAS
 SEQUENCE OF 6-585 FROM N.A.
 "Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10."\,;
 ADLER D.A.,
 KARLSEN
 MEDLINE;
 BU D.-F., TOBIN A.J.;
 MEDLINE; 94375018.
 "Characterization of a linear epitope within the human
 LERNMARK A.
 176
 A41292; F
 M81882; AAA62367.1;

M74826; AAA58491.1;

X69936; CAA49554.1; I

M70435; AAA52513.1;
 DECARBOXYLASE.
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A.E., HAGOPIAN W.A., GRUBI
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 Acad. Sci. U.S.A. 88:8337-8341(1991).
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 Score 155; DB 1;
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 GRUBIN C.E., DUBE S., HEWES S., GRANT F.J.,
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4-AMINOBUTANOATE
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 *FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;

*Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.";

Endocrinology 133:2962-2972(1993).

-!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

-!- CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).

-!- COFACTOR: PYRIDOXAL PHOSPHATE.

-!- COFACTOR: PYRIDOXAL PHOSPHATE.
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 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
(65 KD GLUTAMIC ACID DECARBOXYLASE).
GAD2 OR GAD65.
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
 STRAIN-C57BL/6; T:
MEDLINE; 97115675
ASADA H., KAWAMUR
 LEE D.S., TIAN J., PHAN T., KAUFMAN "Cloning and sequence analysis of a decarboxylase (GAD65).";
 ASADA H., KAWAMURA Y., MARUYAMA K., KUME H., DING R.G., JI F.Y., KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.; "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase (GAD55) maintain normal levels of GAD67 and GABA in their brains
 STRAIN-C57BL/6; TI
MEDLINE; 94032481.
 SEQUENCE
 Neurotransmitter
 PFAM;
 MEDLINE; 94062679
 SEQUENCE OF 175-379
 are susceptible to seizures.";
 SEQUENCE FROM N.A.
 SEQUENCE
 Eukaryota; Metazoa;
 Mus musculus
 176
 щ
 DECARBOXYLASE.
 SIMILARITY: LOCAL TO DOPA DECARBOXYLASE,
 SUBUNIT: HOMODIMER (BY SIMILARITY)
 L16980; AAA93049.1; -.; D42051; BAA22893.1; -.; S67454; CAB32806.1; -. MGI:95634; GAD2.
 PRYFNQLSTGLDMVGLAADW
 PF00282;
 Similarity
20; Conser
 PS00392; DDC_GAD_HDC_YDC;
00282; pyridoxal_deC; 1
nsmitter biosynthesis; Lya;
 Biophys. Res. Commun.
 phosphate;
 Rodentia;
 (Mouse)
 Conservative
 TISSUE-BRAIN;
 TISSUE-BRAIN;
 100.0%;
 396
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65224
 FROM N.A.
 Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
 synthesis: Lyase: Decarboxylase; Multigene family.
 1216:157-160(1993).
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 Score
Pred.
 PYRIDOXAL PHOSPHATE (POTENTIAL).

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I -> S (IN REF. 2).

K -> E (IN REF. 2).

-> S (IN REF. 2).
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-> S (IN
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 229:891-895(1996)
 Mismatches
 155; DB 1;
No. 2.36e-21;
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 encoding glutamate
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01-FEB-1996
 P48318;
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 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence upd
01-FEB-1996 (Rel. 33, Last annotation u
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM
(67 KD GLUTAMIC ACID DECARBOXYLASE).
 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
 SEQUENCE
 Neurotransmitter
Pyridoxal phosph
 GAD1 OR GAD67
 DCE1_MOUSE
 PFAM; PF00282;
 PROSITE; PS00392;
 TISSUE-BRAIN
 SEQUENCE OF 198-403
 KATAROVA Z., SZABO G., MUGNAINI E.
"Molecular identification of the 6:
decarboxylase from the mouse.";
Eur. J. Neurosci. 2:190-202(1990).
 TISSUE-BRAIN;
 SEQUENCE FROM N.A.
 Eutheria;
 Mus musculus (Mouse).
 MEDLINE; 94062679
 184 PRFFNQLSTGLDIIGLAGEW
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 PRYFNQLSTGLDMVGLAADW
 Z49976; CAA90277.1;
S67453; CAB32805.1;
 Similarity 75.0% 15; Conservative
 ; Metazoa;
Rodentia;
 phosphate;
(Rel. 16, Created)
(Rel. 16, Last, sequence update)
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 pyridoxal_deC; 1.
er biosynthesis; Lyase; Decarboxylase;
phate; Multigene family.
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 Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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 Score 135;
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 PYRIDOXAL PHOSPHATE (POTENTIAL).
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 EMBL; M34445; AAC42037.1; -. EMBL; X57572; CAA40800.1; -. EMBL; X57573; CAA40801.1; -. EMBL; M76177; AAA41184.1; -. PIR; A41367; A41367. PIR; A43756; A43756.
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 "Cloning, characterization, and autoimmune recognition of glutamic acid decarboxylase in insulin-dependent diabetes Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).

-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

-i- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE
 PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_deC; 1.
Neurotransmitter biosynthesis; Lyase;
Pyridoxal phosphate; Multigene family.
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 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
 SEQUENCE FROM MEDLINE; 92020
 JULIEN J.F., SAMAMA P., MALLET J.;
"Rat brain glutamic acid decarboxylase sequence cDNA.";
 SEQUENCE FROM N.A. MEDLINE; 90132703.
 "Characterization of a
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 GLUTAMATE DECARBOXYLASE, 67 KD ISOFC (67 KD GLUTAMIC ACID DECARBOXYLASE).
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 MICHELSEN B.K., PETERSEN J.S., BOEL E.,
 J. Neurochem.
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 COFACTOR:
 KD GLUTAMIC
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 SIMILARITY: BELONGS
 SUBUNIT:
 PRFFNQLSTGLDIIGLAGEW
 PRYFNQLSTGLDMVGLAADW
 OR GAD67
 Similarity 75.0%, 15; Conservative
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 ACTIVITY: L-GLUTAMATE PYRIDOXAL PHOSPHATE.
 54:703-705(1990).
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 Res. 8:193-198(1990).
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 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
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 L -> V (IN REF. 2).
F -> S (IN REF. 2).
EH -> AD (IN REF. 2).
AG -> EA (IN REF. 2).
T -> I (IN REF. 2).
FD -> LE (IN REF. 2).
L -> R (IN REF. 2).
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 BU D.-F., ERLANDER M.G., HITZ B.C., T
WAGNER MCPHERSON C.B., EVANS G.A., TO
"Two human glutamate decarboxylasses,
each encoded by a single gane.",
Proc. Natl. Acad. Sci. U.S.A. 89:2115
 Q99259;
Q1-FEB-1996 (Rel. 33, Created)
Q1-FEB-1996 (Rel. 33, Last sequence update)
Q1-OCT-1996 (Rel. 34, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC
(67 KD GLUTAMIC ACID DECARBOXYLASE).
 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Entheria; Cetartiodactyla; Suina; Suidae; Sus.
 GAD1
 PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00782; pyridoxal_dec; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
BINDING 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
 Homo sapiens (Human).

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 Gene 152:257-260(1995).

-i- FUNCTION: CATALYZES THE PRODUCTI
-i- CATALYTIC ACTIVITY: L-GLUTAMATE
-i- COFACTOR: PYRIDOXAL PHOSPHATE.
 "Sequences of two po
 DCE1_HUMAN
 SEQUENCE
 EMBL; D31849; BAA06636.1;
 67-kDa GAD)."
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 SUBUNIT: HOMODIMER (
 SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
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 OR GAD.
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 Similarity
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 Conservative
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 Score 135; I
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 PRODUCTION OF GABA
 89:2115-2119(1992)
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 BU D.-F., TOBIN A.J.;
BU D.-F., TOBIN A.J.;
"The exon-intron organization of the genes two human glutamate decarboxylases (GAD67 at two human glutamate acommon ancestral GAD.";
they derive from a common ancestral GAD.";
 EMBL;
EMBL;
EMBL;
EMBL;
 KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFST E., MUSSEY S.S., POVEY S., CARTER N.D., "Nucleotide sequence and chromosomal assignment of the large isoform of human glutamate decarboxylase. Ann. Hum. Genet. 56:255-265(1992).
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 TISSUE=TESTIS;
MEDLINE; 90355
 CRAM D.S., BARNETT L.D., JOSEPH J.L., HARRISON L.C.; "Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets."; Biochem. Biophys. Res. Commun. 176:1239-1244(1991).
 SEQUENCE FROM N.A.
TISSUE-PANCREATIC ISLETS;
MEDLINE; 93282845.
 YAMASHITA K., CRAM D.S., HARRISON L.C.;
"Molecular cloning of full-length glutamic acid decarboxylase human pancreas and islets.";
Biochem. Biophys. Res. Commun. 192:1347-1352(1993).
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 decarboxylase in male germ cells." Mol. Cell. Biol. 10:4701-4711(1990)
 KAWASAKI E., MORTUCHI R., WATANABE M., SAITOH K., BRU WATI P.C., YAMAGUCHI T., MULLEN Y., BAZAWA S., MIYAW "Cloning and expression of large isoform of glutamic decarboxylase from human pancreatic islet.";
 SEQUENCE FROM N.A. MEDLINE; 93282844.
 SEQUENCE FROM N.A MEDLINE; 94375018
 -!- FUNCTION: CATALYZES THE PRODUCTION
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4
 "Expression of the neurotransmitter-synthesizing
 PERSSON H.,
 SEQUENCE OF 527-594
 SEQUENCE OF 218-397
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 SUBUNIT: HOMODIMER. SIMILARITY: BELONGS
 COFACTOR: PYRIDOXAL PHOSPHATE.
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M81883;
L16888;
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 91248209
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 Biophys. Res. Commun. 192:1353-1359(1993).
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 HOEKFELT T., RITZEN E.M.
 90355986.
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 EMBL; M86522; AAA35900.1;
EMBL; M70434; AAA52512.1;
EMBL; M55574; AAA72938.1;
EMBL; A28074; CAA01913.1;
PIR; PQ0157; PQ0157.
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 KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;
"Gluttamic acid decarboxylase cDNA: nucleotide sequence
enzymatically active fusion protein.";
J. Neurosci. 7:2768-2772(1987)
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-i- CATALYZIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE
 PROSITE; PS00392; DDC_GAD_HDC_YDC; PFAM; PF00282; Pyridoxal_deC; 1. Neurotransmitter biosynthesis; Lya
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PIR; A46758; A46758.

PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_deC; 1.

Neurotransmitter biosynthesis; Lyase; Dev
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Pyridoxal phosphate; Multigene family.
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66824 MW; 3EC20778
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01-FEB-1991 (Rel. 17, Created)
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01-NOV-1995 (Rel. 32, Last annotation updat
GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD)
 PIR; A30999; A30999.
PIR; JH0192; JH0192.
FLYBASE; FB9D0004516; Gad1.
PROSITE; PS00392; DDC_GAD_HCC_YDC;
PFAM; PF00282; pyridoxal_dec; 1.
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 Pyridoxal phosphate.
BINDING 322 3
 EMBL; X76198; CAA53791.1; -.
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 JACKSON F.R., NEWBY L.M., KULKARNI S.J., "Drosophila GABAergic systems: sequence
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
 Drosophila melanogaster (Fruit fly)
 GAD OR GLB.
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 Neurotransmitter biosynthesis; Lyase;
 SEQUENCE FROM N.A.
 102
 185 PRFFNQLSTGLDIIGLAGEW
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 id decarboxylase.",
Neurochem. 54:1068-1078(1990).
FUNCTION: CATALYZES THE PRODUCTION
CATALYTIC ACTIVITY: L-GLUTAMATE = 4
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 SUBUNIT: HOMODIMER. SIMILARITY: BELONGS
 COFACTOR: PYRIDOXAL SUBUNIT: HOMODIMER.
 10
 PHFFNQLSNGLDLISMAGEW 121
 PRYFNQLSTGLDMVGLAADW
 Similarity 55.0%, 11; Conservative
 15;
 Similarity
 90155291.
 510 AA;
 Conservative
 STANDARD;
 74.2%;
 322
57758 MW;
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 the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to licenseeisb-sib.ch).
 STRAIN-ATCC 15692 / MEDLINE; 96100768.
 MURE_PSEAE STANDARD; PRT; 325 AA. Q59650; Q59650; Q1-NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 35, Last sequence update) Q15-JUL-1999 (Rel. 38, Last annotation update) Q15-JUL-1999 (Rel. 38, Last annotation update) Q15-N-ACETYLMURAMOYLA-TRIPEPTIDE SYNTHETASE) (MESO-EC 6.3.2.13) (UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE) (MESO-
 euphyllophytes; Spermate
core eudicots; Rosidae;
 -!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
 "Cloning and characterization of the Pseudomonas aeruginosa encoding penicillin-binding protein 3": antimicrob. Agents Chemother. 39:1871-1874(1995). Antimicrob. Agents Chemother. 39:1871-1874(1995). -i- FUNCTION: CELL WALL FORMATION. DIAMINOPPHELIC ACID ADDIN-1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-GLUTAMATE + MESO-2,6-DIAMINOHEPTANEDIOATE - ADP + ORTHOP
 MURE
 (TRANSAMINASE A).
AAT1 OR ASP5.
 EMBL; X84053; CAA58873.1; 7.

PFAM; PF01225; Mur_ligase; 1.

Peptidoglycan synthesis; Cell
ATP-binding.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 Arabidopsis
 AATM_ARATH
 LIAO X., HANCOCK R.E.W.;
 Bacteria;
 Pseudomonas
 (EC 6.3.2.13) (UDP-N-ACETYLMURAMYL-TRIPEPTIDE DIAMINOPIMELATE-ADDING ENZYME) (FRAGMENT).
SEQUENCE FROM N.A.
 SEQUENCE FROM
 Pseudomonas
 92 RFYGEPSRGLDLIGVTG 108
 N
 DIAMINOHEPTANEDIOATE
 + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
 RYFNQLSTGLDMVGLAA 18
 Similarity
 Proteobacteria;
 108
325
325 AA;
 Conservative
 STANDARD;
 41.9%;
35.3%;
 34215
 PAO1;
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 BULT C.T., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G. BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
 WILKIE S.E., LAMBERT R., WARREN M.J.;

Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-
-CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN

METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.

-i- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE - OXALOACETATE +
 SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 /
MEDLINE; 96337999.
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 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82).
 WILKIE S.E., ROPER J., Submitted (AUG-1994) to
 TISSUE-LEAF; WILKIE S.E.,
 Methanococcus jannaschii.
Archaea; Euryarchaeota; M
 PFAM;
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 Methanococcus
 "Complete genome
jannaschii.";
 199 RYYDPKTIGLDFEGMIAD 216
 Local Similarity
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SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 COFACTOR: PYRIDOXAL PHO
SUBUNIT: HOMODIMER (BY
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 AMINOTRANSFERASES.
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 X81026; CAA56932.1; -.
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 PF00155; aminotran_1; 1.
 peptide; Multigene family
 PS00105; AA_TRANSFER_CLASS_1; 1.
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 Aminotransferase; Pyridoxal phosphate;
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PARMENTIER Y., CRIQUI M.C., DURR A., FLECK J.;

Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND CYCLE RELATED ORGANIC ACIDS: IN PLANTS, IT IS INVOLVED IN METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.

-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE - OXALOAC
 This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf the European Bioinformatics Institute.
 Science 273:1058-1073(1996).
-i- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE "ARCHAEBACTERIAL" MALATE DEHYDROGENASE
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 SCHULTZ C.J.,
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 COFACTOR: PYRIDOXAL PHOSPHATE.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (
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 344 AA;
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186 PROTON-RELAY (POTENTIAL).
189 SUBSTRATE CARBOXYL GROUP
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PROSITE: PS00105; Aminotran_1; 1.

PPAM; PF00155; aminotransferase; Pyridoxal phosphate; Multigene fami
Transferase; Aminotransferase; Pyridoxal phosphate (BY SIMILARITY).

BINDING 251 251 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 HSSP; P00508; 1TAT.

PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.

PRAM; PF00155; aminotran_1; 1.

Transferase; Aminotransferase; Pyridoxal phosphate.

Transferase; Aminotransferase; PyridoxAL PHOSPHATE (BY SIMILARITY).

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SEQUENCE 407 AA; 44507 MW; E5DC8A40 CRC32;
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 P37833;
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P37934 (Rel. 30, Created)
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P37935 (Rel. 30, Last sequence update)
P37935 (Rel. 30, Created)
P3795 (Rel.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 "Characterization and mapping of cDNA encoding aspartate aminotransferase in rice, Oryza sativa L.";
DNA Res. 3:303-310(1996).
PORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-IP FUNCTION: IMPORTANT FOR THE METABOLISM, OF AMINO ACIDS AND KREBS-CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN METABOLISM AND ENERGY METABOLISM.

"IT CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
 SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
MEDLINE; 97191542
SONG J., SASAKI T., MINOBE Y.;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 EMBL; U15033; AAA79370.1; -.
EMBL; Z26740; CAA81411.1; -.
HSSP; P00508; ITAT.
PROSITE; PS00105; AA_TRANSFE
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 Oryza sativa (Rice).
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 EMBL; D14673;
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154 RYYDPATRGLDFQGLLED 171
 Poaceae; Oryza.
 152 RYYDPATRGLDFKGLLED 169
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 SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
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 Statistics:
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| 21 65 41.9 457 10 042425 PLASTIDIC ASPARTATE AM 170CHONDRIAL PROTEIN.  24 64 41.3 675 2 054202 PERI CAPSID PROTEIN (FRAGME 14.3 794 14 09WF20 CAPSID PROTEIN PRECURSOR PROTE 14.3 794 14 09WF20 CAPSID PROTEIN PRECURSOR PROTE 15.4 1.3 794 14 09WF20 CAPSID PROTEIN.  25 64 41.3 794 14 09WF20 CAPSID PROTEIN.  26 41.3 796 14 09WF20 CAPSID PROTEIN.  27 64 41.3 794 14 09WF20 CAPSID PROTEIN.  28 64 41.3 794 14 09WF20 CAPSID PROTEIN.  29 65 40.6 252 2 084983 PHAG.  30 63 40.6 252 2 084983 PHAG.  31 63 40.6 583 5 045986 ZRAD37.4 PROTEIN PRECURSOR PROTEIN.  36 63 40.6 578 14 091508 ASPARTATE AMINOTRANSFE CAPSID PROTEIN PRECURSOR PROTEIN.  37 63 40.6 778 14 091508 CAPSID PROTEIN PRECURSOR PROTEIN.  38 62 40.0 578 14 097723 PROBABLE BETA-1, 3-CLUC SINILAR TO D. DISCOIDE PROTEIN PRECURSOR PROTEIN PROTEIN PRECURSOR PROTEIN PROTEIN PRECURSOR PROTEIN PRECURSOR PROTEIN PRECURSOR PROTEIN PRECURSOR PROTEIN PROTEIN PRECURSOR PROTEIN PROTEIN PRECURSOR PROTEIN PRECURSOR PROTEIN PROTEIN PRECURSOR PROTEIN PROTEIN PROTEIN PR |        |        |        |             |                        |                        |        |                        |        |         |             |                   |             |        |        |           |        |        |         |                     |           |        |                       |                        |           |
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| 41.9 457 10 042425 41.3 670 3 006436 41.3 670 3 006436 41.3 670 3 006436 41.3 670 3 006436 41.3 675 2 054202 41.3 786 14 012792 41.3 786 14 012792 41.3 787 14 028242 41.3 794 14 028242 41.3 794 14 028243 41.3 794 14 028244 41.3 794 14 028244 41.3 794 14 028244 41.3 794 14 028244 41.3 796 14 028244 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 41.3 796 14 028246 | 45     | 44     | 43     | 42          | 41                     | 40                     | 39     | 38                     | 37     | 36      | 35          | 34                | 33          | 32     | 31     | 30        | 29     | 28     | 27      | 26                  | 25        | 24     | 23                    | 22                     | 21        |
| 457 10 042425  PLASTIDIC ASPARTANTE  3 427 10 042803  HITOCHONDRIAL ASPARTANTE  3 670 3 006436  CHROMOSOME XII COSM  3 675 2 054202  PEP1.  3 786 14 012792  CAPSID PROTEIN PR | 61     | 61     | 61     | 61          | 62                     | 62                     | 62     | 62                     | 63     | 63      | 63          | 63                | 63          | 63     | 63     | 64        | 64     | 64     | 64      | 64                  | 64        | 64     | 64                    | 64                     | 65        |
| 10 042425 PLASTIDIC ASPARTATE 11 042803 MITOCHONDRIAL ASPARTATE 12 054202 PEP1. 13 006436 CHROMOSOME XII COSM 2 054202 PEP1. 14 012792 CAPSID PROTEIN (FRA 14 082452 STRUCTURAL PROTEIN PROTEI | 39.4   | •      | ٠      | •           |                        |                        | •      |                        |        |         |             |                   | •           |        |        |           |        |        |         |                     |           |        |                       |                        |           |
| 042425 PLASTIDIC ASPARTATE 042803 MITOCHONDRIAL ASPA 054202 PEP1. 012792 CAPSID PROTEIN (FRA 084452 012792 CAPSID PROTEIN PROTEIN 09WF20 CAPSID PROTEIN 09WF20 CAPSID PROTEIN 09WF20 CAPSID PROTEIN 09WF20 CAPSID PROTEIN 072163 CAPSID PROTEIN 072161 07242 PHAG 07242 PHAG 07242 PHAG 07242 PROBABLE BETA-1,3-C 07724 PROBABLE BETA-1,3-C 07724 PROBABLE BETA-1,3-C 07242 PROBABLE BETA-1,3-C 0724062 URIDINE DIPHOSPHATE 042794 ASPARTATE AMINOTRAN 041199 ASPARTATE AMINOTRAN 041199 ASPARTATE AMINOTRAN 042249 FITAAZ2.21 PROTEIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 797    | 463    | 463    | 412         | 575                    | 513                    | 323    | 294                    | 783    | 778     | 778         | 583               | 409         | 252    | 247    | 816       | 796    | 794    | 794     | 787                 | 786       | 675    | 670                   | 427                    | 457       |
| PLASTIDIC ASPARTATE PLASTIDIC ASPARTATE MITOCHONDRIAL ASPARA CHROMOSOME XII COSM PEP1.  CAPSID PROTEIN (FRASTRUCTURAL PROTEIN CAPSID PROTEIN. CAPSID PRECURSOR PROCESIN. CAPSID PRECURSOR PROFEIN. CAPSID PROTEIN. PHAG. 2K1037.4 PROTEIN. CAPSID PROTEIN PRECURSOR PROFEATOR PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROFEID PROTEIN PRECURSOR PROBABLE BETA-1,3-CAPSID PROTEIN PRECURSOR PROBABLE BETA-1,3-CAPSID PROTEIN PRECURSOR PROTEIN  | 10     | 10     | 10     | 2           | υ                      | Ŋ                      | 14     | N                      | 14     | 14      | 14          | ഗ                 | 10          | N      | N      | 14        | 14     | 14     | 14      | 14                  | 14        | N      | ω                     | 10                     | 10        |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |        |        |        | DIPHOSPHATE | GLUTAMATE DECARBOXYLAS | PUTATIVE SERINE/THREON |        | PROBABLE BETA-1,3-GLUC |        | PROTEIN | POLYPROTEIN | ZK1037.4 PROTEIN. | AMINOTRANSF | PHAG.  |        | PRECURSOR | -      | _      | PROTEIN | STRUCTURAL PROTEIN. | PROTEIN ( | PEP1.  | CHROMOSOME XII COSMID | MITOCHONDRIAL ASPARTAT | ASPARTATE |

## ALIGNMENTS

| OCCUPIED AC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Qy<br>RESULT | ф                        | Que<br>Bes<br>Mat                                                                                                                                                   | SO                                                                                     | 2 2 2                                                             | 38 | 88                                                 | 집                                                          | ₽ ?         | g R                | RN                                                               | 38 | S | GN | E:               | 3 5                                               | ဌ                     | AC t | RESULT                         |
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| 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) 01-NOV-1998 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) | 1 6321       | PREFNQLSTGLDMIGLAGEW 200 | Query Match 92.9%; Score 144; DB 13; Length 590;<br>Best Local Similarity 80.0%; Pred. No. 6.38e-18;<br>Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0; | Lyase; Decarboxylase; Pyridoxal phosphate.  SEQUENCE 590 AA; 66710 MW; 80B66DFF CRC32; | EMBL; AF030355; AAD01902.1; PROSTTE: PS00392: DDC GAD HDC YDC: 1. |    | -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY). | "Characterization of glutamate decarboxylase in chicken."; | WAGBERG F.; | SEQUENCE FROM N.A. | неоднаснае, очитионнее, снастаничае, снастаничае, очитае.<br>[1] |    |   |    | ECARBOXYLASE 67. | Ol-MAY-1999 (TremBurel, 10, Last sequence update) | (TrEMBLrel. 10, Creat |      | T 1 PRET.THTNARY: PRT: 590 AA. |

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 ZENG L.-W., COMERON J.M., CHEN B. Genetica 0.0-0(1997).
EMBL: AF025807: AAB87892.1: -.
HSSP: P06543: 100D.
FLYBASE: FBgn0023295: Dpse\Gad1.
PFAM: PF00282: pyridoxal_deC; 2.
 [1]
SEQUENCE |
MEDLINE;
BOND R.W.
 PFAM; PF00282; pyridoxal_deC; 1.
Lyase: Decarboxylase: Pyridoxal phosphate.
SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;
 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
67KD GLUTAMIC ACID DECARBOXYLASE.
 "Developmentally regulated expression of an exon containing codon in the gene for glutamic acid decarboxylase."; Proc. Natl. Acad. Sci. U.S.A. 87:8771-8775(1990). EMBL; M38350; AAA41185.1; -. PFAM: PF00282; pyridoxal_deC; 1. SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;
 Eukaryota; Metazoa; Arthropoda; Tracheata; Ho
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
 PROSITE; PS00392; DDC_GAD_HDC_YDC;
 EMBL; Y12257; CAA72934.1;
 Submitted
 AUST G.,
 STRAIN-BALB/C;
 Eukaryota; Metazoa;
Eutheria; Rodentia;
 Mus musculus (Mouse)
 008685;
 008685
 SEQUENCE FROM N.A
 SEQUENCE FROM N.A.
 184 PRFFNQLSTGLDIIGLAGEW
 184 PRFFNQLSTGLDIIGLAGEW
 4
 TG., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER ... mitted (APR-1997) to the EMBL/GenBank/DDBJ databases. COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY). SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, TYRDC).
 PRYFNQLSTGLDMVGLAADW
 PRYFNQLSTGLDMVGLAADW
 R.W., WYBORSKI R.J.,
 Similarity 75.0%;
15; Conservative
 15;
 Similarity
 FROM
 91062362
 PRELIMINARY;
 Conservative
 Chordata; Cran
Sciurognathi;
 87.1%;
75.0%;
 87.1%;
75.0%;
 203
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 GOTTLIEB D.I.;
 20
 Score 135;
Pred. No. 1
5; Mismat
 Score 135; DB 11;
Pred. No. 1.10e-15;
 Craniata;
 PRT;
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 Muridae;
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 593 AA
 1.10e-15;
atches 0;
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ae; Murinae;
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O1-NOV-1999 (TYEMBLREL. 12, L
GLUTAMIC ACID DECARBOXYLASE.
UNC-25 OR Y37D8A.23.
 044103 PRELIMINARY;
044103;
01-JUN-1998 (TrEMBLrel. 06, C.
01-JUN-1998 (TrEMBLrel. 12, L.
01-NOV-1999 (TrEMBLrel. 12, L.
GLUTAMIC ACID DECARBOXYLASE ()
 SEQUENCE FROM N.A. C
ZENG L.-W., COMERON J.M., C
Genetica 0:0-0(1997),
EMBL; AF025808; AAB87893.1;
HSSP; P06543; 1QOC.
 STRAIN-BRISTOL;
MEDLINE; 99098940.
JIN Y., JORGENSEN E., HARTWIEG E., HORVITZ H.R.;
"The Caenorhabditis elegans gene unc-25 encodes glutamic decarboxylase and is required for synaptic transmission b synaptic development.";
J. Neurosci. 19:539-548(1999).
 NON_TER
SEQUENCE
 NON_TER
 Eukaryota; Metazoa; Nematoda; Rhabditina; Rhabditoidea; Rhal
 Caenorhabditis elegans.
 Submitted
 BARLOW
 SPECIES=C.elegans;
 SEQUENCE FROM N.A.
 Rhabditina;
 FLYBASE; FBgn0023244; Dsub\Gad1.
PFAM; PF00282; pyridoxal_deC; 2.
 Pterygota; Neoptera; Endopterygota;
 Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tr
 GAD1.
 SEQUENCE
SEQUENCE FROM
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 NON_TER
 Ephydroidea; Drosophilidae; Drosophila
 22
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 PRYFNQLSTGLDMVGLAADW
 PHFFNQLSNGLDLISMAGEW
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 ×.;
 Similarity
11; Conser
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llarity 55.0%;
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 A.
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 41
 CHEN
 oda; Secernentea; Rhabditi: Rhabditidae; Peloderinae;
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 Score 115; DB 5;
Pred. No. 7.32e-11;
8; Mismatches 1
 Score 115; DB 5;
Pred. No. 7.32e-11;
8; Mismatches 1
 PRT;
 В.,
 D75BDC49 CRC32;
 A1EB456F CRC32;
 Tracheata; Hexapoda; Insecta;
 Diptera;
 508
 370
 AA
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 update)
 Rhabditia; Rhabditida,
 update)
 Brachycera; Muscomorpha;
 Length 370;
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 Caenorhabditis
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RESULT 7
ID 770713;
AC P70713;
AC P70713;
DT 01-FEB-1
DT 01-MAY-1
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01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLREL. 10, Last annotation update)
CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)
CYSTEINE-SULFINATE DECARBOXYLASE)
 Q9Y602;
01-NOV-1999
01-NOV-1999
01-NOV-1999
 CYSTEINE CSAD.
 Q9Y602
 NON_TER
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SEQUENCE
 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT J., COULSON
CRAXTON M., DEAR S., DU Z., DUBEN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORRIMORE B., O'CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEE
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
elegans.";
 SPECIES=C. MEDLINE; 9
 STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER; KRATSKIN I.L., YU X., SMUTZER G., DOTY R.L.; SUBMITTER G., COTY-1996) to the EMBO-L-ALANINE STRAINTIC ACTIVITY: 3-SULFINO-L-ALANINE STRAINTIC REPRESENTATION PYRIDOXAL-PHOSPHATE.
 Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Entheria: Rodentia; Sclurognathi; Muridae;
 Nature 368:32-38(1994).
EMBL; AF109378; AAD1958.1; -.
EMBL; AL032626; CAR21537.1; -.
SEQUENCE 508 AA; 57792 MW;
 Homo sapiens (Human)
Eukaryota; Metazoa;
 SEQUENCE FROM N.A.
 100
 46
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 Match
 PRFFNQISCGLDLVSMAGEW
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PRYFNQLSTGLDMVGLAADW
 PRYFNQLSTGLDMVGLAA
 PRFFNQLFSGLDPHALAG
 h 51.6%;
Similarity 61.1%;
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 C.elegans;
94150718.
 999 (TrEMBLrel. 12, Created)
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 78
 1
78
7 AA;
 PRELIMINARY;
 PRELIMINARY;
 Conservative
 pyridoxal_deC;
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9134 MW;
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 Chordata;
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 Score 114;
Pred. No. 1.
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 CRC32;
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 DB 5;
L.26e-10;
 Vertebrata;
 CRC32;
 Vertebrata; Mammalia;
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 Mammalia;
 Rattus
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 SHOWNKEEN
 COULSON A.,
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CYSTEINE SULFINIC A
 Q64577
Q64577;
Q64577;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1999
 Submitted EMBL; AF11
 01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)
(SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
 MEDLINE: 95290499
KAISAKIA P.J., JERKINS A.A., O
"Cloning and characterization
 Eutheria;
[1]
 Homo sapiens (Human) Eukaryota; Metazoa;
 PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
PFAM; PF00282; pyridoxal_dec; 1.
Lyase; Decarboxylase; Pyridoxal phosphate.
SEQUENCE 478 AA; 53725 MW; 4CAC0093 CF
 PRITCHARD J.E., RAMSDEN D.B.;
"Human cysteine sulfinic acid decarboxylase ((
"Human cysteine sulfinic acid decarboxylase ((
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ
EMBL; AF116545; AAD32543.1;
 SEQUENCE FROM TISSUE-BRAIN;
 SEQUENCE FROM N
 Eutheria;
 CSAD.
 STRAIN-SPRAGUE-DAWLEY;
 SEQUENCE FROM N.A.
 Eutheria;
 Eukaryota;
 Rattus norvegicus (Rat).
 SEQUENCE
 PRITCHARD
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 decarboxylase.";
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 PREFNQLESGLDPHALAG
 PRYFNQLSTGLDMVGLAA 18
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 Chordata; Craniata;
Sciurognathi; Murida
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WILSON R., AINSCOUGH R., ANDERSON K.,
BONFIELD J., BURTON J., CONNELL M., C
CRAXTON M., DEAR S., DUR DURBIN R
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 017621
 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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01-JAN-1998 (TrEMBLrel.
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 PFAM; PF00282; pyridoxal_deC; 1.
Lyase; Decarboxylase; Pyridoxal
SEQUENCE 493 AA; 55248 MW; D
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)
 "Human cysteine sulfinic acid decarboxylase (CSAD) relat
submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF116547; AAD32945.1; -
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 CRAXTON M., GARDNER A.,
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 SEQUENCE FROM N.A.
 C29F7.2 PROTEIN
 REYMOND I., SERGEANT A., TAPPAZ M.;
"MOlecular cloning and sequence analysis of the liver cysteine sulfinate decarboxylase (CSD).";
Biochim. Biophys. Acta 1307:152-156(1996).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY-1-- SIMILARITY: BELONGS TO GROUP II DECARBOXYLAS
 Rattus norvegicus
 PROSITE; PS00392; DDC_GAD_HDC_YDC;
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larity 61.1%;
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NELL M., COPSEY T., COOPER J., CC DURBIN R., FAVELLO A., FULTON L. NS T., HILLIER L., JTFB "
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01-MAY-1997 (TrEMBLrel. 03, L
01-NOV-1999 (TrEMBLrel. 12, L
RIBOKINASE (EC 27.1.15).
Escherichia coli
 017620
017620;
017620;
01-JAN-1998
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 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
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CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
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THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M. WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"1.2 M. WEINSTOK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III o
 Nature 368:32-38(1994).
EMBL; Z92827; CABO7326.1;
SEQUENCE 394 AA; 44297
 Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Bacteria; Proteobacteria;
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 Rhabditina;
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MIZOBUCHI K., WORI H., MORI T., MOTOMURA K., NAKADE S., NAKAMURA Y.,

NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,

SIVASUNDARAM S., TAGAMI H., TAKEDA J., TAKEMOTO K., WADA C.,

YAMAMOTO Y., HORIUCHI T.;

"A 460-kb DNA sequence of the Escherichia coli K-12 genome

COLLESPONDING TO THE 40.1-50.0 min region on the linkage map.";

DNA Res. 3:379-392(1996).

EMBL; D90848: BAA15968.1; -.
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052961; O1.NOV-1996 (TrEMBLrel. 01, Created)
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01.NOV-1998 (TrEMBLrel. 08, Last annotation update)
 Escherichia.
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 MEDLINE; 97474264.

PLATER J., STERR W., HAUSMANN M., SCHMITT R.;

"Three genes of a motility operon and their role in flagellar rotary speed variation in Rhizobium meliloti.";

J. Bacteriol. 179:6391-6399(1997).

EMBL: L49337; AAB81407.1; ...
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| S      | ტ        | 6                     | o      | 1.69e+01              | 6         | 1.69e+01              | 1.69e+01 | 1.69e+01              | 1.18e+01             | <u>.</u>              | 1.18e+01             |                       |     |                      | 1.18e+01              |          | . 28   | .776 |                      | 4.01e+00              | 2.77e+00              |  |

## ALIGNMENTS

| RESULT 2 ENTRY TITLE JUNEAU JH0423 ENTRY TITLE ALTERNATE_NAMES Glutamate ORGANISM #formal_n DATE 18-Jun- ACCESSIONS JH0423; A REFERENCE U, Tob #journal Erlander, N; Tob #journal Two genes #cross-references MUID: #accession JH0423 #accession JH0423 #accession JH0423 #accession JH0423                          | Db 32 TYEIAP<br>      <br>  Qy 1 TYEIAP                                     | Query Match<br>Best Local Sim:<br>Matches 20;                                                                                     | ##CGESSION ###STATUS ##molecule. ##residues ##recross-re: CLASSIFICATION SUMMARY                                                                                                                                                              | #authors #journal #title #cross-referen                                                                                                                                                                                                                                                               | RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE                                                                                                                                                 |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ULT 2  JH0423 #type complete  RY  JH0423 #type complete  glutamate decarboxylase (AD65; L-glutamate 1-carboxy-lyase ANISM  #formal_name Rattus norvegicus #common_name Norway rat  E 1-Mar-1992 #sequence_revision 23-Mar-1995 #text_change  ESSIONS JH0422; A60888  ESSIONS JH0422; A60888  ERENCE JH0423  #authors | TYBIAPVEVLLEYVTLKKMR 51<br>                     <br>TYBIAPVEVLLBYVTLKKMR 20 | h 100.0%; Score 155; DB 2; Length 205; Similarity 100.0%; Pred. No. 1.21e-17; 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | ##status preliminary: translated from GB/EMBL/DDBJ##molecule_type mRNA ##resldues 1-205 ##label RES##resldues 1-205 ##label RES##Terences GB:S67454; NID:9456852##CATION #superfamily human glutamate decarboxylase#length 205 #checksum 3167 | authors Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harrison, L.C. journal Endocrinology (1993) 133:2962-2972 Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.  cross-references MUID:94062679 | 167412 #type fragment 65 kda glutamate decarboxylase, brain - mouse (fragment) #formal_name Mus musculus #common_name house mouse 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 167412 153274 |

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 #authors Karlsen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes,
Grant, F.J.; Foster, D.; Lernmark, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform
#toross_references_MUID:92020848
 #journal
#title
 **BRENCE A60888

**Fauthors Chang, Y.C.; Gottlieb, D.I.

**journal J. Neurosci. (1988) 8:2123-2130

**title Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.

**cross-references_MUID:88258610
 #authors
 #accession
 #cross-references MUID:92196068
#accession A41935
 #accession
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'V',191-194,'X',196-203,'XX',206-219;'X',225-234,'X',
##residues

'V',191-194,'X',249-266,'X';524-537,539-543,'V',547-549,

'X',551-553,'X',555-558 ##label CHA

NT This enzyme (GAD) catalyzes the formation of an inhibitory
neurottansmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.

IFICATION #superfamily human glutamate decarboxylase

IFICATION carbon carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 ##residues 1-585 ##label ERL
##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
##experimental_source brain
 ##note
 206 TYEIAPVFVLLEYVTLKKMR 225
 ##experimental_source
 ##residues 1-585 ##label KAR ##cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
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 ##experimental_source brain
 ##residues 1-585 ##label BU1
##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
 ##molecule_type mRNA
 ##status
 ##note
 1 TYEIAPVFVLLEYVTLKKMR 20
 100.0%;
Similarity 100.0%;
 glutamate decarboxylase (EC 4.1.1.15) 2 - human glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Homo sapiens #common_name man 13-May-1992 #sequence_revision 23-Mar-1995 #text_change
 A41292
 A41292
 Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.
 #length
 A60888
 Bu, D.F.; Erlander, M.G.;
 A41935; A41292; S30058; B54778
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 phosphate
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 preliminary
 the authors translated the codon GAT for residue 86\ as His, TCA for residue 198\ as Ala, and CAG for residue
 sequence extracted from NCBI backbone (NCBIP:88007)
 #binding_site pyridoxal phosphate (Lys) (covalent)
 #status predicted
1585 #molecular-weight
 428 as Trp
 D.L.; Wagner-McPherson,
pancreatic islet
 #type complete
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Pred. No. 1.21e-17
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 #contents annotation; intron-exon boundaries

MMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
 #map_position
 #cross-references MUID:94375018
 #accession
 #title
 #gene
 #cross-references MUID:93185681
#accession $30058
 #cross-references MUID:94032481
 #journal
 #authors
 #title
 #journal
 #journal
 #authors
 authors
 ##cross-references GB:L16980; NID:g413867; PIDN:AAA93049.1; PID:g413868
YT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
IFICATION #superfamily human glutamate decarboxylase
 206 TYEIAPVEVLLEYVTLKKMR 225
 ##experimental
 ##residues
 ##residues
 ##molecule_type mRNA
 ##cross-references GDB:128595;
 ##cross-references EMBL:X69936
 ##molecule_type mRNA
 Local
 1 TYEIAPVFVLLEYVTLKKMR 20
 h 100.0%;
Similarity 100.0%;
20; Conservative
 B.; Northemann, W.

Eur. J. Biochem. (193) 212:597-603

Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.
 glutamate decarboxylase (EC 4.1.1.15) 2 - mouse glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase #formal_name Mus musculus #common_name house mouse 20-May-1994 #sequence_revision 23-Mar-1995 #text_change
 Bu, D.F.; Tobin, A.J.
Bu, D.F.; Tobin, A.J.
Benomics (1994) 21:222-228
The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
 Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.I
Biochim. Biophys. Acta (1993) 1216:157-160
Cloning and sequence analysis of a murine of
glutamate decarboxylase (GAD65).
 carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 S38533
 S38533
 S38533
 S38533
 #length 585
 #superfamily human glutamate decarboxylase
 10p11.23-10p11.23
 GDB:GAD2
 A54778
 Mauch,
 GAD
 GAD-65) suggests that they derive from a common ancestral
 phosphate
 18-Jun-1999
 _source pancreatic
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
gth 585 #molecular-weight 65411 #checksum 4799
 1-585 ##label LEE
 6-585 ##label MAU
 preliminary
 Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel, hemann, W.
 #type complete
 Score 155; DB 1;
Pred. No. 1.21e-17;
0; Mismatches 0
 OMIM: 138275
 islet
 0
 Length 585;
 Indels
 cDNA encoding
 Gaps
 0
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393-396
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 #journal
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#title
 #cross-references MUID:94062679 #accession IS3274
 #cross-references MUID:95137399 #accession JC4064
 #authors
 ##molecule_type mRNA
##molecule_type mRNA
##residues 1-585 ##label SUZ
##cross-references DDBJ:D31848; NID:g790964; PIDN:BAA06635.
##cross-references DDBJ:d1007207; PID:g790965
##MOLECUTE__ye.
##residues 1-206 ##label RES
##cross references GB:S67453; NID:g456853
#FICATION #superfamily human glutamate decarboxylase
#Y #length 206 #checksum 3323
 ##molecule_type mRNA
 206 TYEIAPVFVLLEYVTLKKMR 225
 206 TYEIAPVFVLLEYVTLKKMR 225
 Local Similarity 100.0%;
hes 20; Conservation
 ##status
 100.0%;
Local Similarity 100.0%;
les 20; Conservation
 _
 1 TYEIAPVEVLLEYVTLKKMR 20
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 TYEIAPVFVLLEYVTLKKMR 20
 S
 This
 his enzyme catalyzes the conversion of glutamic gamma-amino butyric acid.

N #superfamily human glutamate decarboxylase
 I53274 #type fragment
glutamate decarboxylase, 67K, brain - mouse (fragment)
#formal_name Mus sp. #common_name mouse
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
16-Feb-1997
 Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harrison, L.C. Endocrinology (1993) 133:2962-2972
Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.
 glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig
#formal_name Sus scrofa domestica #common_name domestic pig
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
 carbon-carbon lyase; carboxy-lyase
 Sequences of two porcine 67-kDa GAD).
 Suzuki, R.;
Gene (1995)
 #length 585
 Suzuki
 153274
 JC406
 JC406
 #length 585
 phosphate
 22-Jun-1999
 #domain DOPA decarboxylase binding #status
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
 preliminary; translated from
 #label BIN
 #type complete
 Asami, N.; Amann,
152:257-260
 #molecular-weight 65388
 #molecular-weight 65224
 Score 155;
Pred. No. 1
 Pred.
 Score 155;
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 glutamic acid decarboxylases (65-and
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 DB 2;
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 Length 585
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 #accession S61533
##molecule_type mRNA
##molecule_type mRNA
1-554, 'YQPQGDKANFFRMVISNPAASQSDIDFLTEEIERLGQDL'
 #journal #title
 #journal
#title
 #title Cloning, characterization, and autoimmune recognition of islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.

#cross-references MUID:92020930

#accession A41367
 #accession
 #authors
 #submission
 authors
##molecule_type mRNA ##residues
 214 TYEIAPVFVLMEQITLKKMR 233
 ##experimental_source brain
 ##cross-references EMBL:249976; NID:g886686; PIDN:CAA90277.1;
PID:g886687
 ##experimental_sou
S61533
 ##residues
 ##note
 ##cross-references EMBL:249976
 ##molecule_type mRNA
 17
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 TYEIAPVFVLLEYVTLKKMR 20
 TYEIAPVEVLLEYVTLKKMR 20
 TYEIAPVFVLMEQITLKKMR
 84.5%;
Similarity 85.0%;
17; Conservation
 h 84.5%;
Similarity 85.0%;
17; Conservative
 A41367 #type complete
glutamate decarboxylase (EC 4.1.1.15) 1 - rat
glutamate decarboxylase (AD67; L-glutamate 1-carboxy-lyase
#formal_name Rattus norvegicus #common_name Norway rat
12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
 Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrug Dyrberg, T.; Madsen, O.D. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
 *superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase
 submitted to the EMBL Data Library, June 1995
 Katarova, Z.; Szabo, G.; Mugnaini,
Eur. J. Neurosci. (1990) 2:190-202
Molecular identification of the 62
decarboxylase from the mouse.
 glutamate decarboxylase (EC 4.1.1.15) 62K isc glutamic acid decarboxylase #formal_name Mus musculus #common_name house 19-Mar-1997 #sequence_revision 25-Apr-1997 #t
 $61534; $61533
$61534
 A41367; A43756; JH0195
A41367
 Szabo,
 S6153
 #length 585 #molecular-weight 65381 #checksum
 22-Jun-1999
 18-Jun-1999
 source brain
 1-593 ##label
 the differences at the carboxyl end are frameshift error
 l-585 ##label
 <u>ه</u>
 #type complete
 36
 Score 131; DB 2;
Pred. No. 2.07e-12;
2; Mismatches 1
 Pred.
2; N
 Score 131; DB 2;
Pred. No. 2.07e-12;
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 4.1.1.15) 62K isoform -
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 Length 206
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 E.; Moldrup,
 Greenspan, R.J
 #text_change
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 ##label
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 ACCESSIONS
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 Matches
 Query Match 84.5%;
Best Local Similarity 85.0%;
 Matches
 *journal
 404
 #authors Julien, J.F.; Samama, P.; Mallet, J.
#journal J. Neurochem. (1990) 54:703-705
#journal Rat brain glutamic acid decarboxylase sequence
#title cloned cDNA.
#cross-references MUID:90132703
 #cross-references MUID:93080286
#accession S48135
 #authors
 #cross-references MUID:91014554
#accession A43756
 #accession
 #journal
 #authors
 ##molecule_type mRNA

##residues 1-102,'V',104-283,'S',285-286,'AD',289-343,'EA',346,'I',

##cross-references GB:X57572; NID:g75185; PIDN:CAA40800.1; PID:g75186

NT This enzyme (GAD) catalyzes the formation of an inhibitory

neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;

it has several isoforms, each encoded by a separate gene.

IFICATION #superfamily human glutamate decarboxylase

Carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 ##cross-references EMBL:222750
##cross-references EMBL:222750
#superfamily human glutamate decarboxylase
RX #length 593 #molecular-weight 66952 #chec
 ###Cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184
##note the authors translated the codon TGT for residue 412 as
Ser and TCT for residue 413 as Cys
 ##residues
 214 TYEIAPVFVLMEQITLKKMR 233
 ##cross-references GB:M76177; NID:g204227; PIDN:AAA41184.1; PID:g204228
NCE A43756
214 TYEIAPVFVLMEQITLKKMR 233
 ##molecule_type mRNA
 ##molecule_type mRNA
 1 TYEIAPVFVLLEYVTLKKMR 20
 Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.
Brain Res. Mol. Brain Res. (1990) 8:193-198
Characterization of a cDNA coding for rat glutamic acid
 glutamate decarboxylase (EC 4.1.1.15) - human
#formal_name Homo sapiens #common_name man
14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
 #status
#length 593 #r
 Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D. Ann. Hum. Genet. (1992) 56:255-265
Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate
 S48135
 JH0195
 JH0195
 Kelly, C.D.; Edwards, Y.; Johnstone,
 Conservative
 Conservative
 decarboxylase.
 decarboxylase.
 07-May-1999
 phosphate
 1-593 ##label KEL
 #binding_site pyridoxal phosphate (Lys) (covalent)
 preliminary
 84.5%;
 #type complete
 #molecular-weight 66640
 Score 131; DB 2; Length 593; Pred. No. 2.07e-12;
 Score 131; DB 1; Length 593; Pred. No. 2.07e-12;
 2;
 Mismatches
 Mismatches
 66952 #checksum
 A.P.; Harfst,
 #checksum
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##experimental_source pancreatic TH0806
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 SUMMARY
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 #journal
#title
 #accession
 #authors Kawasaki, E.; Moriuchi, R.; Watanabe, M.; Saitoh, K.
Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen,
Akazawa, S.; Miyamoto, T.; Nagataki, S.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
#title Cloning and expression of large isoform of glutamic
decarboxylase from human pancreatic islet.
#cross-references_MUID:93282845
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 #authors
 #accession
 #submission
 #cross-references MUID:92196068
 #authors
 ##molecule_type mRNA
1-17,'N',19-30,'N',32-67,'K',69-115,'L',117-154,'T',
##residues 156-301,'C',303-476,'G',478-491,'G',493-594 ##label
 ##cross-references GB:S61898; NID:g385310;
##experimental_source pancreatic islet
 ##cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936
 214 TYEIAPVFVLMEQITLKKMR 233
 ##molecule_type mRNA
##residues
 ##note
 ##residues
 ##molecule_type mRNA
 ##cross-references EMBL:Z22750
##note this is an unpublished revision
 Local
 1 TYEIAPVEVLLEYVTLKKMR
 \vdash
 11
 10
 TYEIAPVEVLLEYVTLKKMR
 h 84.5%;
similarity 85.0%;
17; Conservative
 16-Feb-1997
S51776
 B41935 #type complete
glutamate decarboxylase (EC 4.1.1.15) 1 - human
glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
#formal_name Homo sapiens #common_name man
#formal_name Homo sapiens #common_name #formate reference $48135

**superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase #length 593 #molecular-weight 66946 #chec
 Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119 Two human glutamate decarboxylases, 65-kDa GAD and GAD, are each encoded by a single gene.
 Johnstone, A. submitted to the
 glutamate decarboxylase (EC 4.1.1.15) - human #formal_name Homo sapiens #common_name man 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
 JH0805
 Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;
Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin
 18-Jun-1999
B41935; JH0805; JH0806; A61406; PQ0157; PQ0158;
 S51776
 JH0805
 A41935
 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
 A36463; A54778
 1-594 ##label
 1-593 ##label
 sequence extracted from NCBI backbone (NCBIP:88006)
 #type complete
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 Pred.
2; M
 Score 131; DB 2; Le
Pred. No. 2.07e-12;
2; Mismatches 1;
 EMBL Data Library, May 1993
 BUI
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 Yamaguchi, T.; Mullen,
 66946 #checksum
 PIDN:AAB26938.1; PID:g385311
 Length 593;
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 Indels
 Saitoh, K.;
 sequence from
 B41367;
 4842
 67 - kDa
 Gaps
 Charles
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##molecule_type mRNA
##residues 527-594 ##label PER
##cross-references GB:M35574; NID:g182929; PIDN:AAA72938.1; PID:g182930
REFERENCE A54778
 ##molecule_type mRNA

##residues 218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,

'D',331-338,'L',340-390,'S',392-397 ##label CR2

##cross-references GB:M70435; NID:g182941; PIDN:AAA52513.1; PID:g182942

##experimental_source pancreatic islet

REFERENCE A41367
 #contents
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 REFERENCE
 REFERENCE
 #journal
#title
 #authors Yamashita, K.; Cram, D.S.; Harrison, L.C.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title Molecular cloning of full-length glutamic acid decarboxylase
67 from human pancreas and islets.
#cross-references.MUID:93282844
 S.; Skog, S.; Hoekfelt, T.; Ritzen, E.M.
#journal Mol. Cell. Biol. (1990) 10:4701 4711
#title Expression of the neurotransmitter-synthesizing e
glutamic acid decarboxylase in male germ cells.
#cross-references_MUID:90355986
 #accession B4136/
##molecule_type mRNA
 #cross-references MUID:91248209
#accession PQ0157
 #title
 #journal
 #cross-references MUID:94375018
 #cross-references MUID:92020930
 #journal
 #cross-references MUID: 92065769
 #authors
 #journal
 #authors
 #title
 #authors
 authors
 ##cross-references GB:M70434
##experimental_source brain
cession PQ0158
 ##residues
 ##molecule_type mRNA
##residues 218-463 ##label CR1
 ##experimental_source brain
 ##molecule_type mRNA
 experimental_source pancreatic islet
ts annotation; intron-exon organization
This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic aci
it has several isoforms, each encoded by a separate gene. GAD
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
 Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyrberg, T.; Madsen, O.D.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
Cloning, characterization, and autoimmune recognition of islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
 Cram, D.S.; Barnett, L.D.; JOSEPH, J.L.; MILLERY, Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.
 Bu, D.F.; Tobin, A.J.

Genomics (1994) 21:222-228

The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestra
 Kelly, C.; Carter, N.D.; Johnstone,
Lancet (1991) 338:1468-1469
Cloning of large isoform of human by
decarboxylase
 Persson, H.; Pelto-Huikko,
 A61406
 A36463
 62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 ##label KEL
 317-482,'R',484-594 ##label MIC
 M.; Metsis,
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 #authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal J. Neurosci. (1987) 7:2788-2772
#title Glutamic acid decarboxylase cDNA: nucleotide sequence
encoding an enzymatically active fusion protein.
#cross-references_MUID:87310623
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#accession
 #accession
 #submission
 #authors
 #accession
 #submission
 #authors
 ##cross-references EMBL:Z22750; NID:g298098; PIDN:CAA80435.1;
PID:g298099
FICATION #superfamily human glutamate decarboxylase
 ##cross-references GDB:119244; OMIM:266100 p_position 2q31-2q31
 ##residues 1-594 ##label KOB
##cross-references GB:M18629; NID:g163858; PIDN:AAA51430.1;
#NCE A45671
 215 TYEIAPVFVLMEQITLKKMR 234
 ##molecule_type mRNA
 ##residues
 ##molecule_type mRNA
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 1 TYEIAPVFVLLEYVTLKKMR 20
 12
 TYEIAPVFVLLEYVTLKKMR
 TYEIAPVEVLMEQITLKKMR 234
 Similarity
 glutamate decarboxylase (EC 4.1.1.15) 1 - cat glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase #formal_name Felis silvestris catus #common_name domestic c31_Dec-1993 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999.
 #superfamily human glutamate decarboxylase
alternative splicing; carbon-carbon lyase; carboxy-lyase;
phosphoprotein; pyridoxal phosphate
 submitted to GenBank, A46758
 A46758; A45671
A46758
 S51775
S51775
 Johnstone, A. submitted to the EMBL Data Library, May 1993 S51775
 glutamate decarboxylase (EC 4.1.1.15) - human formal_name Homo sapiens fcommon_name man 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999
 #status predicted
#length 594 #molecular-
 carbon-carbon lyase; carboxy-lyase
#length 594 #molecular-weight 66973 #checksum
 Kobayashi, Y.; Kaufman, D.L.; Tobin,
 GDB:GAD1;
 Conservative
 Conservative
 1-594 ##label JOH
 #binding_site pyridoxal phosphate (Lys) (covalent)
 preliminary
 84.5%;
 84.5%;
 #type complete
 #type complete
 #molecular-weight 66924 #checksum 6189
 Score 131; DB 1;
Pred. No. 2.07e-12;
2; Mismatches 1
 Score 131; DB 2;
Pred. No. 2.07e-12;
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 Length 594;
 Length 594
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 PID:g163859
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ACCESSIONS
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 #gene
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 Matches
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 #authors
 215 TYEIAPVFVLMEQITLKKMR 234
 ##experimental_source brain
This enzyme catalyzes the conversion of glutamic acid into
gamma-amino butyric acid.
FICATION #superfamily human glutamate decarboxylase
 ##note this sequence has been revised in reference A46758
This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic it has several isoforms, each encoded by a separate gene.
 ##residues 1-594 ##label SUZ
##cross-references DDBJ:D31849; NID:g790966; PIDN:BAA06636.1;
PID:d1007208; PID:g790967
 ##molecule_type mRNA
 215 TYEIAPVFVLMEQITLKKMR 234
 y Match 84.5%;
Local Similarity 85.0%;
 ##residues
 1 TYEIAPVFVLLEYVTLKKMR 20
 1 TYEIAPVFVLLEYVTLKKMR 20
 15
 14
 A30999 #type complete
glutamete decarboxylase (EC 4.1.1.15) C1 -
(Drosophila melanogaster)
L-glutamate 1-carboxy-lyase
#formal_name Drosophila melanogaster
26-Oct-1989 #sequence_revision 23-Mar-1995
Jackson, F.R.; Newby, L.M.; Kulkarni, J. Neurochem. (1990) 54:1068-1078
 Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M. Gene (1995) 152:257-260
Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).
 glutamate decarboxylase (EC 4.1.1.15) 67K chain - pig
#formal_name Sus scrofa domestica #common_name domestic pig
30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
22-Jun-1999
 *superfamily human glutamate decarboxylase carbon-carbon lyase; carboxy-lyase; phospho
 JH0192; PS0301; A30999
 carbon-carbon lyase; carboxy-lyase
 JC4065
 #status predicted
#length 594 #molecular-weight 66824
 #length 594 #molecular-weight 66894 #checksum
 Conservative
 Conservative
 18-Jun-1999
 phosphate
 \# domain\ DOPA\ decarboxylase\ binding\ \# status\ predicted \# label\ BIN
 #binding_site pyridoxal phosphate (Lys) (covalent)
 1-558, 'RGTRPTFSGWSSRTQLLHSPILTSSSRR' ##label KO2
 #type complete
 Score 131; DB 2; Length 594; Pred. No. 2.07e-12;
 Score 131; DB 1; Pred. No. 2.07e-12;
 Mismatches
 Mismatches
 Length 594;
 1; Indels
 phosphoprotein; pyridoxal
 #checksum
 Indels
 #text_change
 fruit fly
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 0;
 5491
 Gaps
 Gaps
 acid;
 0;
 0;
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##cross-references FlyBase:FBgn0004516
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
 COMMENT
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 뮍
 GENETICS
Search completed: Tue Mar
Job time : 8 secs.
 SUMMARY
 FEATURE
 Matches
 Query Match 79.4%;
Best Local Similarity 75.0%;
 #title Drosophila GABAergic systems; sequence and expression of glutamic acid decarboxylase.
#cross-references_MUID:90155291
 #gene
 #accession
 132 TYEIAPVFILMENVVLTKMR 151
 ##residues 1-510 ##label
##cross-references GB:X76198;
 ##residues
 ##molecule_type mRNA
 ##molecule_type mRNA
 1 TYEIAPVFVLLEYVTLKKMR
 idues 156-200, 'F', 202-300, 'K', 302-384, 'L', 386-510 ##label JA2 This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutanic acid; it has several isoforms, each encoded by a separate gene.
 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
#length 510 #molecular-weight 57758 #checksum 3194
 FlyBase:Gadl
 PS030
 Conservative
 phosphate
 7 21:52:32 2000
 20
 Score 123; DB 1;
Pred. No. 1.02e-10;
 2
 JAC
NID:g433082; PIDN:CAA53791.1; PID:g433083
 Mismatches
 Length 510
 Indels
 0
 Gaps
 0
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| CEZ_RAT CEZ_HUMAN CEZ_TEG CEZ_HUMAN CEZ_TEG CEZ_HUMAN CLUTAMATE CEL_MOUSE CLUTAMATE CEL_RAT CEL_HONG CELHUMAN CLUTAMATE CELLFIG CELHUMA CLUTAMATE CELLFIG CLUTAMATE CUANINE NU BI_LYMST CUANINE CUANINE CUANINE CUANINE CUANINE CUANINE CHAI CHAI CHAI CHAI CHAI CHAI CHAI CHAI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | e greater than or equal to the score of the result is derived by analysis of the total score distribut summaries  Summaries  Query Ouery Ouery Ouery Ouery One Match Length DB ID Description | e: #wiss-prot38 1:swissprot ics: Mean 31.080; Variance 42.635; scale 0.729 red. No. is the number of results predicted by chance | nce: 155 nce: 1 TYEIAPVFVLLEYVTLKKMR 20 ng table: PAM 150 Gap 15 hed: 8229 segs 29864866 resi processing: Minipulm Match 08 Listing first 45 summarie | Copyright (c) 1993-1998 University of Edinburgh, University of Edinburgh (1-20) from US08981824.pep |  |
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| Q05683;  | DCE2_     |            | 45                     | 44                     | 43         | 42                     | 41                     | 40         | 39                     | 38                    | 37                     | 36            | 35                     | 34         | 33                                           | 32                     | 31                     | 30                     | 29                     | 28                     | 27         | 26                    | 25                     | 24                     |  |
| FEB-1996 | 1<br>RAT  |            | 59                     | 59                     | 60         | 60                     | 60                     | 60         | 60                     | 60                    | 61                     | 61            | 61                     | 61         | 62                                           | 62                     | 62                     | 62                     | 62                     | 62                     | 62         | 63                    | 63                     | 63                     |  |
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| rea      | ,,        |            | Ь                      | Н                      | Ь          | Н                      | ш                      | Н          | Н                      | ட                     | Н                      | ப             | ш                      | Ь          | <u>,                                    </u> | ᆫ                      | ш                      | ш                      | ᆫ                      | μ                      | <b> </b> 3 | <b>-</b>              | $\vdash$               | 1                      |  |
| Created) | PRT; 5    | ALIGNMENTS | CDA2_YEAST             | YJ71_YEAST             | ITA2_DROME | AC15_MOUSE             | PC4_RAT                | PC4_MOUSE  | CKR1_MACMU             | CFXQ_GUITH            | CFAB_MOUSE             | CYB_PARTE     | NU1M_DROSU             | CNTF_HUMAN | POLG_TBEVH                                   | POLG_TBEVW             | YDJK_ECOLI             | CBG_SHEEP              | CKR1_HUMAN             | YG1I_YEAST             | SEGB_BPT4  | RRPO_CNV              | SYD_METTH              | GBI_ASTPE              |  |
|          | .85 AA.   |            | CHITIN DEACETYLASE 2 P | HYPOTHETICAL 30.2 KD P |            | ACTIVATOR 1 140 KD SUB | INTERFERON-RELATED PRO | ERFERON-RE | C-C CHEMOKINE RECEPTOR | CFXQ PROTEIN HOMOLOG. | COMPLEMENT FACTOR B PR | CYTOCHROME B. | NADH-UBIQUINONE OXIDOR | н          |                                              | GENOME POLYPROTEIN [CO | HYPOTHETICAL METABOLIT | CORTICOSTEROID-BINDING | C-C CHEMOKINE RECEPTOR | HYPOTHETICAL 33.3 KD P |            | PROBABLE RNA-DIRECTED | ASPARTYL-TRNA SYNTHETA | GUANINE NUCLEOTIDE-BIN |  |
|          |           |            | 2.06e+01               | :                      | 1.41e+01   |                        | 1.41e+01               | 1.41e+01   | 1.41e+01               |                       | სე                     | 9.57e+00      | ຫຼ                     | 9.57e+00   |                                              | 6.48e+00               | 6.48e+00               | 6.48e+00               | 6.48e+00               | 6.48e+00               | 6.48e+00   | 4.36e+00              | 4.36e+00               | 4.36e+00               |  |

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Query Match
Best Local s
Matches 2
 EMBL; M72422; AAA63488.1; -.

PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.

PFAM; PF00282; pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase; Decarboxylase;

Pyridoxal phosphate; Multigene family.

BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).

SEQUENCE 585 AA; 65402 MW; E35D601A CRC32;
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 "Two genes encode distinct glutamate decarboxylases.";
Neuron 7:91-100(1991),
-i- FUNCTION: CHILIYZES THE PRODUCTION OF GABA.
-i- CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).
-i- COFACTOR: PYRIDOXAL PHOSPHATE.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBUNIT: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
 MEDLINE; 91299343.
ERLANDER_M.G., TILLAKARATNE N.J., FELDBLUM S., PATEL N.,
 SEQUENCE FROM N.A.
TISSUE=HIPPOCAMPUS;
MEDLINE; 91299343.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 GAD2 OR GAD65
 01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
(65 KD GLUTAMIC ACID DECARBOXYLASE).
 Rattus norvegicus (Rat).
 DECARBOXYLASE.
h 100.0%;
Similarity 100.0%;
20; Conservative
Score 155; DB 1; Length 585; Pred. No. 6.44e-21; 0; Mismatches 0; Indels
 Mammalia;
Rattus.
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0;

Gaps

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TYEIAPVFVLLEYVTLKKMR

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RESULT 2

RESULT 2

AC P48321;
AC P48321;
AC P48321;
AC P48321;
AT D1-FEB-199
D7 01-FEB-199
D7 01-FEB-199
D7 01-FEB-199
D8 GLUTAMATE
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GN GAD2 OR GGI
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OC Eukaryota
OC Eukaryota
OC EUKARYOTA
OC EUTACIA;
RN GAD2 OR GGI
OS SUS SCROF,
RN SUZUKI R.
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Best Local Similarity 100.0%;
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01-FEB-1996 (Rel. 33, Last annotation u
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM
(65 KD GLUTAMIC ACID DECARBOXYLASE).
 Detween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
 PFAM; PF00282; Pyridoxal_dec; 1.

Neurotransmitter biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family.

BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
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 ВU
 GAD2 OR GAD65.
Homo sapiens (Human)
 Sus scrofa (Pig).
 MEDLINE; 92196068
 SEQUENCE FROM N.A.
 Eutheria;
 Eukaryota; Metazoa;
 DCE2_HUMAN
 SUZUKI R., ASAMI N., AMANN E., WAGATSUMA
"Sequences of two porcine glutamic acid o
 TISSUE-BRAIN;
 SEQUENCE FROM N.A.
 Eukaryota; Metazoa;
 (65 KD GLUTAMIC ACID DECARBOXYLASE).
 206 TYEIAPVFVLLEYVTLKKMR
 D -F ,
 TYEIAPVEVLLEYVTLKKMR
 D31848; BAA06635.1; -.
TE; PS00392; DDC_GAD_HDC_YDC;
 95137399.
 Primates;
 ; Metazoa; Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae; Sus.
 ERLANDER
 ASAMI N.,
 585 AA;
 STANDARD;
 STANDARD;
 M.G.,
 Catarrhini;
 65388 MW;
 Chordata; Craniata; Vertebrata; Mammalia;
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 225
 Pred.
0; 1
 Score 155; DB 1;
Pred. No. 6.44e-21;
 B.C.,
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 F3E9BD88
 Hominidae;
 Mismatches
 TILLAKARATNE N.J.,
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 decarboxylases
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 4.1.1.15) (GAD-65)
 0;
 Length 585;
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 Mammalia;
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 GAD, HDC
 CO(2)
 a collaboration
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 Gaps
 D.L.,
 AND
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RESULT ID DO AC Po

DCE2\_MOUSE P48320; 035519;

PRT;

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 В
 Query Match
Best Local S
Matches 2
 PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
PFAM; PF00282; pyridoxal_deC: 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
BINDING 396
9YRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32;
 PIR;
PIR;
 EMBL; M81882; AAA62367.1;
EMBL; M74826; AAA58491.1;
EMBL; X69936; CAA49554.1;
EMBL; M70435; AAA52513.1;
 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
 -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HI
 "The exon-intron organization of the genes (GAD1 and two human glutamate decarboxylases (GAD67 and GAD65) they derive from a common ancestral GAD."; Genomics 21:222-228(1994).
 WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.,
"Two human glutamate decarboxylases, 65-kDa GAD and
each encoded by a single gene.",
proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
 sera from insulin-dependent diabetes mellitus Eur. J. Biochem. 212:597-603(1993).
 64-kDa glutamic acid decarboxylase and its autoimmune recognition
 KARLSEN A.E., HAGOPIAN W.A., GRUBI
ADLER D.A., BARMEIER H., MATHEWES
 SEQUENCE FROM N.A.
TISSUE=PANCREATIC ISLETS;
 SEQUENCE FROM N.A. MEDLINE; 94375018.
 NORTHEMANN W.;
 MAUCH L.,
 MEDLINE; 93185681.
 SEQUENCE OF 6-585 FROM N.A.
 "Cloning and primary structure of a human islet isoform of glutamic
 MEDLINE;
 LERNMARK A.
 206 TYEIAPVFVLLEYVTLKKMR
 Characterization of a linear epitope within the human pancreatic
 ۳
 DECARBOXYLASE.
 decarboxylase from chromosome 10.";
. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).
 TYEIAPVFVLLEYVTLKKMR
 A41292; A41292.
PQ0158; PQ0158.
 h 100.0%;
Similarity 100.0%;
20; Conservative
 92020848
 ABNEY C.C.,
 TOBIN A.J.;
 BERG H.,
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 225
 ALT_INIT
 Score 155; DB 1;
Pred. No. 6.44e-21;
0; Mismatches 0
 GRUBIN C.E., DUBE S., HEWES S., GRANT F.J.,
 SCHERBAUM W.A., LIEDVOGEL
 (See http://www.isb-sib.ch/announce/
 There are no rest
 Usage
 AND TO PLP-TYPE HISTIDINE
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 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC
(55 KD GLUTAMIC ACID DECARBOXYLASE).
 pyridoxal phosph
 EMBL;
 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
 This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo
 tissues of mouse and rat.";
Endocrinology 133:2962-2972(1993).
Endocrinology 133:2962-2972(1993).
-!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBUNIT: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
 FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.; "Localization and quantitation of expression of two glutamate decarboxy ase genes in pancreatic beta-cells and other periphe
 STRAIN=C57BL/6; TI
MEDLINE; 94032481.
LEE D.S., TIAN J.,
 BINDING
 MEDLINE; 94062679.
FAULKNER-JONES B.E.,
 Biochem.
 ASADA H., KAWAMURA Y., MARUYAMA K.,
KANBARA N., KUZUME H., SANBO M., YA
 STRAIN=C57BL/6; TISSUE=BRAIN; MEDLINE; 97115675.
 "Cloning and sequence analysis of a murine decarboxylase (GAD65).";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 PFAM;
 EMBL;
 TISSUE-BRAIN;
 are susceptible to seizures.";
 SEQUENCE
 GAD2 OR GAD65
 SEQUENCE OF
 "Mice lacking
(GAD65) maint
 SEQUENCE FROM
 206
 \vdash
 DECARBOXYLASE.
 TYEIAPVFVLLEYVTLKKMR
TYEIAPVEVLLEYVTLKKMR
 L16980; AAA93049.1; -. D42051; BAA22893.1; -. S67454; CAB32806.1; -.
 PF00282;
 N., KUZUME H., SANBO M., YAGI T., OBATA K.; acking the 65 kDa isoform of glutamic acid decarboxylase maintain normal levels of GAD67 and GABA in their brains
 Similarity
 PS00392; DDC_GAD_HDC_YDC; 1.
00282; pyridoxal_deC; 1.
usmitter biosynthesis; Lyase;
l phosphate; Multigene family.
 1 phosphate;
396 39
259 25
319 31
325 32
499 49
 Biophys. Res. Commun. 229:891-895(1996)
 Biophys.
 175-379 FROM N.A.
 (Mouse)
 GAD2
 396
319
325
499
6522
 TISSUE=BRAIN;
 100
 .0%;
 1216:157-160(1993).
20
 W.
 225
 Score
Pred.
0; M
 agreement (See http://www.isb-sib.ch/announce/
 PYRIDOXÂL PHOSPHATE (POTENTIAL).

F -> S (IN REF. 2).

I -> S (IN REF. 3).

K -> E (IN REF. 2).

P -> S (IN REF. 2).

; 9BE5C088 CRC32;
 ght. It is produced through Bioinformatics and the EM
 ≥ 155; DB 1; Len
. No. 6.44e-21;
. ~~+~hes 0;
 KUME H., DING R.G.,
 Decarboxylase;
 4.1.1.15) (GAD-65)
 cDNA encoding
 Usage
 Length 585;
 Indels
 Mus.
 Mammalia;
 peripheral
 and
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 RESULT
 Query Match
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 Matches
 P48318;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4:1.1.15) (GAD-67)
 DCE1_RAT
P18088;
01-NOV-1990
01-NOV-1990
01-FEB-1996
 PFAM; PF00282; pyridoxal_dec; 1.

Meurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family,
BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
CONFLICT 234 234 E -> K (IN REF. 2).
CONFLICT 258 258 S -> T (IN REF. 1).
CONFLICT 360 360 D -> S (IN REF. 1).
SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;
 decarboxylase genes in pancreatic beta-
tissues of mouse and rat.";
Endocrinology 133:2962-2972(1993).
-!- FUNCTION: CATALYZES THE PRODUCTION
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4
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 EMBL; S67453; CAB328
MGD; MGI:95632; GAD1
 EMBL; 249976; CAA90277.1; -. EMBL; S67453; CAB32805.1; -.
 Eukaryota; Metazoa;
Eutheria; Rodentia;
 Mus musculus (Mouse)
 DCE1_MOUSE
 :
 FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.; "Localization and quantitation of expression of two gldecarboxylase genes in pancreatic beta-cells and other
 MEDLINE;
 SEQUENCE OF 198-403
 decarboxylase from
 KATAROVA Z., SZABO G., MUGNAINI I "Molecular identification of the decarboxylase from the mouse.":
 SEQUENCE, FROM N.A.
 TISSUE-BRAIN;
 TYRDC)
 SUBUNIT: HOMODIMER (BY SIMILARITY) SIMILARITY: BELONGS TO GROUP II DE
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Pred. No. 6.
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 Mismatches
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 OF.
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.98e-15;
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Best Local
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CONFLICT
 EMBL; M34445; AAC42037.1; -.
EMBL; X57572; CAA40800.1; -.
EMBL; X57573; CAA40801.1; -.
EMBL; M76177; AAA41184.1; -.
EMBL; A41367; A41367.
 "Cloning, characterization, and autoimmune recognition.";
glutamic acid decarboxylase in insulin-dependent diabetes mellitus.";
proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
-i- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-i- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
 Rattus norregicus (Rat).
Rattus norregicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 PFAM; PF00282; pyridoxal_deC; l.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
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 GLUTAMATE DECARBOXYLASE, (67 KD GLUTAMIC ACID DEC.
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 MADSEN O.D.;
 "Rat brain glutamic pDNA.":
 MEDLINE; 90132703
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 MEDLINE; 91014554
WYBORSKI R.J., BOI
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 PFAM; PF00282;
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 Brain Res. Mol. Brain
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 "Characterization of a
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 214 TYEIAPVFVLMEQITLKKMR
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 SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
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A43756; A43756.
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AG -> EA (IN REF. 2).
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67 KD GLUTAMATC ACID DECARBOXYLASE).
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BU D.-F., ERLANDER M.G., HITZ B.C., 7
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"Two human glutamate decarboxylases,
each encoded by a single gene.";
Proc. Natl. Acad. Sci. U.S.A. 89:211:
 GAD1
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 -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANC
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
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 -!- SIMILARITY: BELONGS TYRDC).
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 KAWASAKI E., MORIUCHI R., WATANABE M., SAITOH K., BRU WATT P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAN "Cloning and expression of large isoform of glutamic decarboxylase from human pancreatic islet.";
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TISSUE-PANCREATIC
MEDLINE; 93282845.
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PERSSON H.,
 "Cloning and partial nuc decarboxylase cDNA from
 YAMASHITA K., CRAM D.S., HARRISON L.C.; "WAMACHITA K., CRAM D.S., HARRISON L.C.; "Molecular cloning of full-length glutamic acid decarboxylase human pancreas and islets."; Biochem. Biophys. Res. Commun. 192:1347-1352(1993).
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"Nucleotide sequence and chromosomal assignment of the large isoform of human glutamate decarboxylase.
Ann. Hum. Genet. 56:255-265(1992).
 "Expression of the neurotransmitter-synthesizing
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 FUNCTION: CATALYZES THE PRODUCTION CATALYTIC ACTIVITY: L-GLUTAMATE = 4 COFACTOR: PYRIDOXAL PHOSPHATE. SUBUNIT: HOMODIMER.
 SIMILARITY: BELONGS
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 M81883;
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 ive from a common ancestral GAD.";
21:222-228(1994).
 H., PELTO-HUIKKO M., HOEKFELT T., RITZEN
 Biophys. Res.
 93080286
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 PEAKMAN M.,
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AAA62368.1;
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AAB26938.1;
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GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM
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BINDING
 EMBL; M86522; AAA35900.1;
EMBL; M70434; AAA52512.1;
EMBL; M55574; AAA72938.1;
EMBL; A28074; CAA01913.1;
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PIR; A46758; A46758.
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PFAM; PF00282; pyridoxal_deC; 1.

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 JACKSON F.R., NEWBY L.M., KULK
"Drosophila GABAergic systems:
 Eukaryota; Metazoa; Arthropoda; Tracheata; H
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 Drosophila melanogaster (Fruit fly)
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Neurochem. 54:1068-1078(1990).
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 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE)
-!- SIMILARITY: BELONGS TO THE UPF0077 (PECM) FAMILY.
 Nature 388:539-547(1997).
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 01-APR-1993 (Rel. 25, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GUANINE NUCLECTIDE-BINDING PROTEIN G(I), ALPH
CYCLASE-INHIBITING GALPHA PROTEIN).
 EMBL; L18922; AAC41538.1; HSSP; P10824; 1AS3. PFAM; PF00503; G-alpha; 1
 SEQUENCE FROM N.A.
STRAIN-OREGON RED; TISSUE-CENTRAL
MEDLINE; 94138304.
"Molecular cloning of G protein alpha
nervous system of the mollusc Lymnaea
FLBS Lett. 314:215-219(1992).
 MEDLINE; 93106153.
KNOL J.C., WEIDEMANN
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 J. Physiol. (Paris)
-!- FUNCTION: GUANI
 Planorbidae;
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 Lymnaea stagnalis (Great pond
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 transmission.
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 DURGERIAN S.,
 Helisoma trivolvis (Snail).
Eukaryota; Metazoa; Mollusca;
 Lymnaeidae;
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 294 TYEEAAAYIQLQFENLNKKK
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 SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOT SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. S
 FUNCTION: GUANINE NUCLE INVOLVED AS MODULATORS
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 Metazoa;
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 Lymnaea
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 acid and GTP-binding proteins in
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 PLANTA
 ADP-ribosylation; Multigene
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 Gastropoda;
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 Gastropoda; Pulmonata; Basommatophora;
 PRT;
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 FOULGER D., ERRINGTON Submitted (AUG-1997) t
 SEQUENCE
 GTP-binding;
 HSSP;
 EMBL;
 SEQUENCE
 Bacillus/Staphylococcus
 Bacteria; Firmicutes;
 Bacillus subtilis
 ATP-DEPENDENT
 MOD_RES
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 PFAM; PF00503; G-alpha; 1

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 294 TYEEAAAYIQLQFENLNKKK
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LGER D., ERRINGTON J.;

IGER D., ERRINGTON J.;

mitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

FUNCTION: CRITICAL ROLE IN RECOMBINATION AND DNA REPAIR. HEIF

PROCESS HOLLIDAY JUNCTION INTERMEDIATES TO MATURE PRODUCTS

CATALYSING BRANCH MIGRATION. HAS A DNA UNWINDING ACTIVITY

CHARACTERISTIC OF A DNA HELICASE WITH A 3' TO 5' POLARITY.

CHARACTERISTIC OF A DNA (Y-DNA) (BY SIMILARITY).
 SIGNALING SYSTEMS.
FUNCTION: THE G(I) PROTEINS ARE I ADENYLATE CYCLASE: THEY INHIBIT TARENERGIC STINULI.
SUBUNIT: G PROTEINS ARE COMPOSED
 SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, 1) THE ALPHA CHAIN CONTAINS THE GUANNIE NUCLEOTIDE BIND: SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY (GLICOTIVE)
 FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (GINVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS
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European Bioinformatics Institute. There a
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$27013; $27013
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 1 45.28;
Similarity 35.08;
7; Conservative
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 Bacillus/Clostridium group;
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MYRISTATE (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).
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01-AUG-1988 (Rel. 08, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUCCINATE DEHYDROGENASE CYTOCHROME B-558 SUBUNIT.
 EMBL; Y13937; CAA74246.1; -.
EMBL; Z99112; CAB13460.1; -.
SUBTILIST; BG13399; RECG.
PFAM; PF00270; DEAD; 1.
PFAM; PF00271; helicase_C; 1.
Helicase; DNA repair; ATP-binding; DNA recombination; NP_BIND 284 291 ATP (POTENTIAL).
SITE 385 388 DEQH BOX.
SEQUENCE 682 AA; 78140 MW; DFC00437 CRC32;
 MEDIINE: 87250294.
MELIN L., MAGNUSSON K., RUTBERG L.;
"Identification of the promoter of the
" Bacteriol. 169:3232-3236(1987).
 WIPAT A., CARTER N., BRIGNELL C.S., GUY J.B., PIPER K., SANDERS J., EMMERSON P.T., HARWOOD C.R.;
"The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus subtilis chromosome containing genes responsible for stress responses, the utilization of plant cell walls and primary metabolism.";
 entities requires a license agreement (S or send an email to license@isb-sib.ch).
 FRIDEN
"Role c
 MAGNUSSON K., PHILIPS M.K., GUEST J.R., RUTBERG "Nucleotide sequence of the gene for cytochrome subtilis succinate dehydrogenase complex.";
J. Bacteriol. 166:1067-1071(1986).
 SEQUENCE FROM N.A. STRAIN=168 / PY79; MEDLINE; 86223767.
 DHSC
 SEQUENCE OF 1-13 FROM N.A. MEDLINE; 87250294.
 PHILLIPS M.K., HEDERSTEDT L., HASNAIN S., RUTBERG L., GU
"Nucleotide sequence encoding the flavoprotein and iron:
protein subunits of the Bacillus subtilis PY79 succinate
 MEDLINE; 97124191.
WIPAT A., CARTER N.,
 dehydrogenase complex.";
J. Bacteriol. 169:864-873(1987).
 MEDLINE;
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 dicrobiology 142:3067-3078(1996).
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 Similarity 52.9% 9; Conservative
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us group; Bacillus.
in Bacillus subtilis cytochrome b558 for haem
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 Score 68; DB 1; I
Pred. No. 5.63e-01;
 PRT;
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 binding and assembly of succinate: quinone oxidoreductase (complex II).";

MOI. Microbiol. 4:1045-1056(1990).

-i- FUNCTION: DI-HEME CYTOCHROME OF THE SUCCINATE DEHYDROGENASE COMPLEX. THE MID-POINT REDOX POTENTIAL IS +65MV.

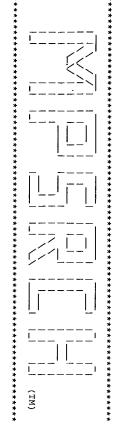
-i- PATHMAY: TRICARBOXYLIC ACID CYCLE.

-i- SUBUNIT: PART OF AN ENAYME COMPLEX CONTAINING THREE SUBUNITS:

A FLAVOROTEIN, AN IRON-SULFUR PROTEIN AND CYTOCHROME B-558.
 TRANSMEM
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 EMBL; M13470; AAA22745.1; -.
EMBL; Z75208; CAA99546.1; -.
EMBL; M15753; AAA22749.1; -.
EMBL; Z99118; CAB14805.1; -.
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 SIMILARITY: TO CYTOCHROME B FROM W.SUCCINOGENES FUMARATE REDUCTASE.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Run on: Tue Mar 7 21:51:53 2000; MasPar time 9.59 Seconds 144.620 Million cell updates/sec

Title: >US-08-981-824-6
Description: (1-20) from US08981824.pep
Perfect Score: 155
Sequence: 1 TYEIAPVFVLLEYVTLKKMR 20
Scoring table: PAM 150
Gap 15

Tabular output not generated.

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 30.016; Variance 47.115; scale 0.637

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1.56e-17<br>1.95e-12<br>1.95e-12<br>3.22e-12<br>3.22e-12<br>3.22e-12<br>3.22e-12<br>5.29e-12<br>6.29e-12<br>6.29e-11<br>1.68e-10<br>2.11e-08<br>8.76e-08<br>8.76e-08<br>8.76e-08<br>8.76e-08<br>3.59e-07<br>5.73e-07                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Pred. No.      |

| 4.4<br>4.5             | 43       | 42            | 41                     | 40                | 39       | 38            | 37                     | 36        | 35            | 34                     | ω<br>ω   | 32                     | 31                     | 30            | 29                | 28          | 27        | 26                     | 25     | 24                     | 23                     | 22                     | 21                     |
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| 41.3<br>41.3           |          | Ľ             | 41.9                   | 41.9              | •        | 41.9          | 42.6                   |           | 42.6          | •                      | 43.9     | 43.9                   | 43.9                   |               | 43.9              | 4           | <u>ب</u>  | <u>ب</u>               | 7      | 51.0                   | 4.                     | 4.                     | ω.                     |
| 1956 5<br>3414 14      |          |               |                        |                   |          |               |                        |           |               |                        |          |                        |                        |               |                   |             |           |                        |        |                        |                        | 08                     |                        |
| Q04956<br>Q9WBS4       | Q13308   | Q9WV72        | Q26058                 | 017124            | 075618   | 060737        | Q9ZI94                 | 004459    | 032057        | Q25294                 | Q25272   | 094994                 | Q9Z2K0                 | Q9Z1L3        | 044648            | Q41760      | Q9XDB4    | 067128                 | Q9ZJZ2 | Q9W658                 | Q24062                 | Q9XY41                 | Q9XTP4                 |
| ATPASE 1. POLYPROTEIN. | ≫        | REPEAT-CONTAI | PUTATIVE SERINE PROTEI | F31F4.16 PROTEIN. | FLDED-1. | KE05 PROTEIN. | PUTATIVE HISTIDINE KIN | F21J9.21. | YRZF PROTEIN. | INTEGRAL MEMBRANE PROT | ORF G.   | NONSENSE-MEDIATED MRNA | DEATH EFFECTOR DOMAIN- | DEDD PROTEIN. | K07C6.15 PROTEIN. | PERMEASE 1. | NA SYNTHA | HYPOTHETICAL 49.7 KD P | •      | GLUTAMATE DECARBOXYLAS | GLUTAMATE DECARBOXYLAS | GLUTAMATE DECARBOXYLAS | GLUTAMIC ACID DECARBOX |
|                        | 8.94e+00 | -             |                        | •                 | 8.94e+00 |               | 6.17e+00               | 6.17e+00  |               |                        | 2.91e+00 |                        |                        |               | 2.91e+00          |             | .35e+0    | ò                      | . 80e  |                        | . 4 6e                 |                        | •                      |

## ALIGNMENTS

| RESU<br>ID<br>AC<br>DT                                                                                                          | Qy<br>Qy                  | Qu<br>Ма                                                                                                                                                      | SQ                    | A A                                        | 另                           | S C | 88                                                                    | 38                                                 | R                           | 꿈                       | RA | R R                | R | გ                                        | 8                                                                 | 3 8                                                                 | G<br>N | DE                | Ϋ́                 | T               | ΡŢ                                   | A t                       | ijĘ                             | RESULT |
|---------------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|--------------------------------------------|-----------------------------|-----|-----------------------------------------------------------------------|----------------------------------------------------|-----------------------------|-------------------------|----|--------------------|---|------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------|--------|-------------------|--------------------|-----------------|--------------------------------------|---------------------------|---------------------------------|--------|
| O08685 PRELIMINARY; PRT; 593 AA. O08685; O1-JUL-1997 (TrEMBLrel. 04, Created) O1-JUL-1997 (TrEMBLrel. 04, Last sequence update) | 2 TYEVAPVEVLLEYVTLKKMR 21 | Query Match 98.7%; Score 153; DB 13; Length 232; Best Local Similarity 95.0%; Pred. No. 1.56e-17; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | 232 23<br>E 232 AA; 2 | Lyase; Decarboxylase; Pyridoxal phosphate. | _GAD_HDC_YD<br>_xal_deC; 1. |     | -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND | -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY). | the developing zebrafish."; | quence and expression c | -  | MEDLINE: 98295903. |   | rinoidea; Cyprinidae; Rasborinae; Danio. | Neoptervq11; Teleoste1; Euteleoste1; Ostariophys1; Cypriniformes; | Bukarvota: Metazoa: Chordata: Craniata: Vertebrata: Actinontervoid: |        | ATE DECARBOXYLASE | 99 (TrEMBLrel. 12, | (TrEMBLrel. 08, | 01-NOV-1998 (TrEMBLrel. 08, Created) | FINDERSTANDANT, FINE, 636 | OG3275 DREITMINARY. DRT. 232 AA | in 1   |

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 BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases molecular phylogeny and evidence for a new GAI Mol. Biol. Evol. 16:397-404(1999).
EMBL; AF043267; AAD22713.1; -.
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 EMBL; Y12257; CAA72934.1; -. PROSITE; PS00392; DDC_GAD_HDC_YDC;
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 TISSUE=BRAIN;
 SEQUENCE FROM N.A.
 Macrouridae;
 Neopterygii;
 Coryphaenoides armatus.
Eukaryota; Metazoa; Chordata;
 GAD65
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 SEQUENCE
 PFAM; PF00282; pyridoxal_deC; 1.
Lyase; Decarboxylase; Pyridoxal phosphate.
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Mus musculus (Mouse)
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eostei; Paracanthopterygii; Gadiformes;
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No. 1.18e-12;
 niata; Vertebrata;
Muridae; Murinae;
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SEQUENCE
 Pseudemys scripta (Slider turtle).
Eukaryota; Metazoa; Chordata; Cran
Cryptodira; Testudinoidea; Emydida
 Lyase.
 BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D. PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases (GAD) molecular phylogeny and evidence for a new GAD paral mol. Biol. Evol. 16:397
 GAD65
 BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., I PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases (GAD) in molecular phylogeny and evidence for a new GAD paralog Mol. Biol. Evol. 16:397-404(1999).

EMBL, AF043265; AAD22711.1;
 01-NOV-1999
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 Pseudemys scripta (Slider turtle).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Cryptodira; Testudinoidea; Emydidae; Trachemys.
 GAD65
 GLUTAMATE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
 GLUTAMATE
 SEQUENCE
 EMBL; AF043273; AAD22719.1;
 TISSUE=BRAIN;
MEDLINE; 9926
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 GAD67.
Gallus
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
 NON_TER
 BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.; "Multiplicity of glutamic acid decarboxylases molecular phylogeny and evidence for a new GAI Mol. Biol. Evol. 16:397-404(1999).

EMBL; AF043270; AAD22716.1; ".
 Poephila guttata (Zebra finch) (Taeniopygia guttata).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Passeriformes; Estrildidae; Estrildinae; Taeniopygia.
 01-NOV-1999 (TrEMBLrel. 12, Created)
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GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT)
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 BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP : PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
"Multiplicity of glutamic acid decarboxylases (molecular phylogeny and evidence for a new GAD Mol. Biol. Evol. 16:397-404(1999).
 EMBL; AF043272; AAD22718.1; -.
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MEDLINE; 9926
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 "Characterization of glutamate decarboxylase in chicken submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC.
SEQUENCE FROM N.A. WATT S.D., SPITZER
 Batrachia;
 Xenopus
 GAD.
 EMBL; AF017266; AAC24327.1; PROSITE; PS00392; DDC_GAD_HDC_YDC; PFAM; PF00282; Pyridoxal_deC; 1.
 SEQUENCE FROM N.A. MEDLINE; 98295903.
 Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
 GLUTAMATE
 PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
Lyase; Decarboxylase; Pyridoxal phosp
SEQUENCE 590 AA; 66710 MW; 80B661
 EMBL; AF030355; AAD01902.1;
 Eukaryota;
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 Lyase;
 MARTIN S.C., HEINRICH G., SANDELL J.H "Sequence and expression of glutamic the developing zebrafish.";
J. Comp. Neurol. 396:253-266(1998).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY-!- SIMILARITY: BELONGS TO GROUP II D
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 Decarboxylase; Pyridoxal
 laevis (African clawed frog).
ta; Metazoa; Chordata; Craniata;
ia; Anura; Mesobatrachia; Pipoid
 h 82.6%;
Similarity 80.0%;
16; Conservative
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 98 (TrEMBLrel. 08, Created)
98 (TrEMBLrel. 08, Last sequence update)
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DECARBOXYLASE (EC 4.1.1.15) (FRAGMENT).
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ID DECARBOXYLASE.
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 Cyprinidae;
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 Teleostei;
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 81.9%;
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 Euteleostei;
 Euteleostei; Ostariophysi; Rasborinae; Danio.
 MW;
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3; N
 Score 127; DB 13;
Pred. No. 8.70e-12;
2; Mismatches 1
 (Zebra danio).
Craniata; Vertebrata;
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 80B66DFF CF
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 nniata; Vertebrata;
Pipoidea; Pipidae;
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II DECARBOXYLASES
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No. 5.29e-12
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GLUTAMIC ACII
 Eukaryota; Me
Pterygota; Ne
Ephydroidea;
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044102
 FLYBASE;
PFAM; PF
 Eukaryota;
Pterygota;
 GLUTAMIC
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SEQUENCE
 HSSP;
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 PROSITE; PS00392; DDC_GAD_HDC_YIPFAM; PF00282; pyridoxal_deC; 1. Lyase; Decarboxylase; Pyridoxal
 EMBL;
 Submitted (OCT-1995) to -!- COFACTOR: PYRIDOXAL -!- SIMILARITY: BELONGS TYRDC).
 EMBL;
HSSP;
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EMBL; AF025808; AAB8
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 Ephydroidea;
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 3 L.-W., COMERON J.M., C
etica 0:0-0(1997).
L; AF025807; AAB87892.1;
P; P06543; 100D.
 YEIAPVFVLLEYVTLKKMR
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 U38225;
 SE; FBgn0023244; Dsub\Gad1.
PF00282; pyridoxal_deC; 2.
 P06543; 1QOC
 PF00282;
 Similarity 75.0% 15; Conservative
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CID DECARBOXYLASE
 Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
 pseudoobscura (Fruit fly)
 Neoptera;
 Metazoa; Arthropoda;
 subobscura
 563 AA;
 (TrEMBLrel.
 (TrEMBLrel.
 PRELIMINARY;
 PRELIMINARY;
 TrembLrel. 06, (TrembLrel. 06, ITrembLrel. 12, ITrembLrel. 12, ID DECARBOXYLASE
 optera; Endopterygota; Diptera;
Drosophilidae; Drosophila.
 Conservative
 AAA96273.1;
pyridoxal_deC;
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 pyridoxal_deC;
 AAB87893.1; -.
 AAB87892.1;
 370
 78.1%;
75.0%;
 79.4%;
78.9%;
 J.M.,
 41887 MW;
 64095 MW;
 (Fruit
 the EMBL/GenBank/DDBJ databases PHOSPHATE (BY SIMILARITY). TO GROUP II DECARBOXYLASES (DDC
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 HDC_YDC;
 Last sequence up Last annotation (FRAGMENT).
 Last sequence up Last annotation (FRAGMENT).
 Created)
 Score 121; DB 5;
Pred. No. 1.68e-10;
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 Pred.
 Score
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 CBBB0C98 CRC32;
 Tracheata;
 Mismatches
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No. 6.29e-11;
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 DECARBOXYLASES (DDC,
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RESULT
AC 06
 D Q64611 PRELIMINAL.,

C Q64611,
DT Q1-NOV-1996 (TIEMBLIFEL O1, Created)
DT Q1-NOV-1996 (TIEMBLIFEL O1, Last sequence update)
DT Q1-NOV-1999 (TIEMBLIFEL O1, Last annotation update)
DT Q1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
DE CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)

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 MEDLINE; 96283809.

REYMOND I., SERCEANT A., TAPPAZ M.;

"Molecular cloning and sequence analysis (
"Molecular cloning and sequence analysis (
liver cysteine sulfinate decarboxylase (C:
liver cysteine sulfinate 1307:152-156(1996)

Biochim. Biophys. Acta 1307:152-156(1996)

-:- COFACTOR: PYRLDOXAL PHOSPHATE (BY SIM

-:- SIMILARITY: BELONGS TO GROUP II DECAP
 LT 13

O64577.

O1-NOV-1996 (TIEMBLIEL 01, Created)
O1-NOV-1996 (TIEMBLIEL 01, Last sequence update)
O1-NOV-1999 (TIEMBLIEL 12, Last annotation update)
O1-NOV-1999 (TIEMBLIEL 12, Last annotation update)
CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)
(SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE)
 NON_TER
 MEDLINE; 95
KAISAKIA P.
 PEAM; PF00282; pyridoxal_deC;
Lyase; Decarboxylase; Pyridoxa
SEOHENDE
 EMBL;
 "Cloning and characterization decarboxylase.";
Biochim. Biophys. Acta 1262:79
 Eukaryota; Metazoa; Chordața; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 SEQUENCE FROM N.A. MEDLINE; 96283809.
 SEQUENCE
 STRAIN-SPRAGUE-DAWLEY;
 SEQUENCE FROM
 Rattus norvegicus (Rat)
 Eutheria;
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 TYEIAPVFVLLEYVTLKKMR
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 M64755; AAC42063.1; TE; PS00392; DDC_GAD_
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oa; Chordata; Cran
ia; Sciurognathi;
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75.08;
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53725 MW; 4
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Pred. No. 2.11e-08;
Pred. ---+ches 3;
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thi; Muridae;
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No. 1.68e-10;
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 HDC
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 rat
 Gaps
 Gaps
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RESULT 15
ID Q9Y602;
AC Q9Y602;
AC Q9Y602;
DT 01-NOV-1999 (TIEMBLrel. 12, Created)
DT 01-NOV-1999 (TIEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TIEMBLrel. 12, Last annotation update)
DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.
GN CSAD.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali
CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RR TISSUE-ERAON N.A.
RT TISSUE-BRAIN;
RA PRITCHARD J.E., RAMSDEN D.B.;
RA PRITCHARD J.E., RAMSDEN D.B.;
RA PRITCHARD J.E., RAMSDEN D.B.;
SOUBLE G (DEC-1998) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 267 AA; 30264 MW; A3475A7D CRC32;
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Search completed: Tue Mar 7 21:52:06 2000 Job time : 13 secs.
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 Query Match 69.7%; Score 108; DB 4; Length 267; Best Local Similarity 70.0%; Pred. No. 8.76e-08; Matches 14; Conservative 3; Mismatches 3; Indels
 Query Match 71.6%; Score 111; DB 11; Length 493; Best Local Similarity 75.0%; Pred. No. 2.11e-08; Matches 15; Conservative 2; Mismatches 3; Indels
 TISSUE~BRAIN;
PRITCHARD J.E.;
PRITCHARD J.E.;
"Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 1.";
submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF116545; AAD32543 1; -
EMBL; AF116545; AAD32543 1; -
EMBL; AF116545; AAD32543 1; -
EMBL; AF116545; AAD32543 MW; A3475A7D CRC32;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 EMBL: X94152; CAA63868.1; -- PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
PFAM: PF00282; pyridoxal_deC; 1.
Lyase: Decarboxylase: Pyridoxal phosphate.
SEQUENCE 493 AA: 55248 MW; D7A66D9A CRC32;
 117 TYEIAPVFVLMEEEVLRKLR 136
 1 TYEIAPVFVLLEYVTLKKMR 20
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 Gaps
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